

GenCore version 5.1.6  
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OM protein - protein search, using sw model  
Run on: February 23, 2005, 20:48:35 ; Search time 132 Seconds  
(without alignment)  
1189.967 Million cell updates/sec

Title: US-10-621-485A-1  
Perfect score: 2550  
Sequence: 1 MSDVAIVKEGWLHKGVEIK.....VDSERPFPQFSYASGTA 480

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1380268 seqs, 327241040 residues

Total number of hits satisfying chosen parameters: 1380268

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:  
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2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
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20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	2550	100.0	480	17	US-10-621-485A-1
2	2550	100.0	492	10	US-09-955-999-96
3	2544	99.8	480	9	US-09-771-161A-223
4	2544	99.8	480	9	US-09-970-000-4
5	2544	99.8	480	10	US-09-526-043-14
6	2544	99.8	480	14	US-10-060-065-18
7	2544	99.8	480	14	US-10-059-585-39
8	2544	99.8	480	15	US-10-394-322A-1
9	2544	99.8	480	15	US-10-217-574-31
10	2544	99.8	480	15	US-10-217-555-31
11	2544	99.8	480	16	US-10-701-490-4
12	2544	99.8	480	16	US-10-713-678-2
13	2544	99.8	480	16	US-10-746-545-36

14	2544	99.8	524	14	US-10-103-256-11	Sequence 11, Appl
15	2544	99.8	524	15	US-10-365-348-11	Sequence 11, Appl
16	2544	99.8	726	14	US-10-072-036-71	Sequence 71, Appl
17	2544	99.8	727	14	US-10-072-036-139	Sequence 139, Appl
18	2509	98.4	480	16	US-10-713-678-6	Sequence 6, Appl
19	2494	97.8	480	9	US-09-205-658-157	Sequence 157, Appl
20	2494	97.8	480	10	US-09-663-693-157	Sequence 157, Appl
21	2161.5	84.8	417	16	US-10-713-678-4	Sequence 4, Appl
22	2128.5	83.5	488	16	US-10-322-281-413	Sequence 413, Appl
23	2126.5	83.4	480	10	US-09-526-043-13	Sequence 13, Appl
24	2126.5	83.4	480	15	US-10-394-568-11	Sequence 11, Appl
25	2126.5	83.4	481	15	US-10-394-568-12	Sequence 2, Appl
26	2126.5	83.4	481	15	US-10-394-322A-2	Sequence 32, Appl
27	2126.5	83.4	481	15	US-10-217-574-32	Sequence 32, Appl
28	2126.5	83.4	481	15	US-10-217-555-32	Sequence 416, Appl
29	2105.5	82.6	479	9	US-09-771-161A-246	Sequence 246, Appl
30	2105.5	82.6	479	9	US-09-771-161A-247	Sequence 247, Appl
31	2105.5	82.6	479	9	US-09-771-161A-248	Sequence 248, Appl
32	2105.5	82.6	479	15	US-10-394-322A-3	Sequence 3, Appl
33	2105.5	82.6	479	15	US-10-217-574-33	Sequence 33, Appl
34	2105.5	82.6	479	15	US-10-217-555-33	Sequence 33, Appl
35	2008.5	78.8	465	10	US-09-526-043-2	Sequence 2, Appl
36	2008.5	78.8	465	15	US-10-394-568-2	Sequence 2, Appl
37	2008.5	78.8	465	15	US-10-394-568-12	Sequence 12, Appl
38	1989.5	78.0	454	10	US-09-526-043-17	Sequence 17, Appl
39	1692	66.4	320	14	US-10-116-722A-7	Sequence 7, Appl
40	1671	65.5	320	14	US-10-116-722A-5	Sequence 5, Appl
41	1573	61.7	300	16	US-10-664-421-84	Sequence 84, Appl
42	1552.5	60.9	335	16	US-10-746-545-24	Sequence 24, Appl
43	1552.5	60.9	335	16	US-10-746-545-37	Sequence 37, Appl
44	1552.5	60.9	336	15	US-10-217-574-21	Sequence 21, Appl
45	1552.5	60.9	336	15	US-10-217-555-21	Sequence 21, Appl

## ALIGNMENTS

RESULT 1  
US-10-621-485A-1  
; Sequence 1, Application US/10621485A  
; Publication No. US20050014682A1  
; GENERAL INFORMATION:  
; APPLICANT: MUECKLER, MIKE  
; APPLICANT: HRESKO, RICHARD  
; APPLICANT: MURATA, HARUHIKO  
; TITLE OF INVENTION: CELL-FREE ASSAY FOR INSULIN SIGNALING  
; FILE REFERENCE: 56029/41936  
; CURRENT APPLICATION NUMBER: US/10/621.485A  
; CURRENT FILING DATE: 2003-07-16  
; NUMBER OF SEQ ID NOS: 1  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 1  
; LENGTH: 480  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-621-485A-1

Query Match 100.0%; Score 2550; DB 17; Length 480;  
Best Local Similarity 100.0%; Pred. No. 2.6e-165;  
Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MSDVAIVKEGWLHKGVEIKTRPRYFLKNDGTFIGYKERPDVDQREAPLNFSVAQC 60  
Db 1 MSDVAIVKEGWLHKGVEIKTRPRYFLKNDGTFIGYKERPDVDQREAPLNFSVAQC 60  
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RESULT 2  
US-09-955-999-96  
; Sequence 96, Application US/09955999  
; Publication No. US20030036505A1  
; GENERAL INFORMATION:  
; APPLICANT: Barash et al.  
; TITLE OF INVENTION: Signal Transduction Pathway Component Polynucleotides, Polypeptide  
; FILE REFERENCE: PT086F1  
; CURRENT APPLICATION NUMBER: US/09/955,999  
; CURRENT FILING DATE: 2001-09-20  
; PRIOR APPLICATION NUMBER: 60/234,997  
; PRIOR FILING DATE: 2000-09-25  
; NUMBER OF SEQ ID NOS: 139  
; SOFTWARE: Patent in ver. 2.0  
; SEQ ID NO 96  
; LENGTH: 492  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-955-999-96  
Query Match 100.0%; Score 2550; DB 10; Length 492;  
Best Local Similarity 100.0%; Pred. No. 2,7e-165;  
Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 433 LSPFPKQVTSSETDTRYFDEEFTAQMITITPPQDDSMCEVDSESRPHFPQFSYASGTA 492  
RESULT 3  
US-09-771-161A-223  
; Sequence 223, Application US/09771161A  
; Patent No. US20020110811A1  
; GENERAL INFORMATION:  
; APPLICANT: LEVINE, et al.  
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES  
; FILE REFERENCE: 802620-2005.1  
; CURRENT APPLICATION NUMBER: US/09/771,161A  
; CURRENT FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: 09/724,676  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: 136776  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 135619  
; PRIOR FILING DATE: 2000-04-12  
; NUMBER OF SEQ ID NOS: 273  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 223  
; LENGTH: 480  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-771-161A-223

Query Match 99.8%; Score 2544; DB 9; Length 480;  
Best Local Similarity 99.8%; Pred. No. 6,7e-165;  
Matches 479; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 4  
US-09-970-000-4  
; Sequence 4, Application US/09970000  
; Patent No. US20020127214A1  
; GENERAL INFORMATION:  
; APPLICANT: Hemmings, Brian Arthur

TITLE OF INVENTION: Rac-Protein Kinase as Therapeutic Agent  
Or In Diagnostics  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESS: No. US2002012714A1arties Patent and Trademark Department  
STREET: 564 Morris Avenue  
CITY: Summit  
STATE: NJ  
COUNTRY: USA  
ZIP: 07901-1027  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/970,000  
FILING DATE: 03-Oct-2001  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US/09/068,702  
FILING DATE: 13-May-1998  
APPLICATION NUMBER: PCT/EP96/04810  
FILING DATE: 11-May-1996  
APPLICATION NUMBER: GB 9523379.7  
FILING DATE: 16-No. US2002012714A1-1995  
APPLICATION NUMBER: GB 9525704.4  
FILING DATE: 15-Dec-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Furman, Diane E.  
REGISTRATION NUMBER: 31,104  
REFERENCE/DOCKET NUMBER: 4-20635/A/PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908) 522-6924  
TELEFAX: (908) 522-6955  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 480 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-09-970-000-4

Query Match 99.8%; Score 2544; DB 9; Length 480;  
Best Local Similarity 99.8%; Pred. No. 6.7e-165;  
Matches 479; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 MSDVAIVKGEWLKRGGEYIKTRPRYFLKNDGTFIGYKERPDQVDQREAPLNPFSAQC 60  
Db 1 MSDVAIVKGEWLKRGGEYIKTRPRYFLKNDGTFIGYKERPDQVDQREAPLNPFSAQC 60  
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Db 61 QLMKTERPRNTFIIRCLQWTVIERTPHVETPEEREETTAIQTVDGLKKQEEEMDF 120  
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Db 121 RSGSPSDNSGAEEMVSLAKPKHRTVMNEFYLLKLGKGTGKVLVKEKATGRYAMKI 180  
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RESULT 6  
US-10-060-065-18  
; Sequence 18, Application US/10060065  
; Publication No. US20030017480A1  
; GENERAL INFORMATION:  
; APPLICANT: Toshio Ota

Db 361 ILKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLS 420  
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RESULT 5  
US-09-526-043-14  
; Sequence 14, Application US/09526043  
; Publication No. US20030100049A1  
; GENERAL INFORMATION:  
; APPLICANT: Guo, Kun  
; APPLICANT: Pagnoni, Marco  
; APPLICANT: Clark, Kenneth  
; APPLICANT: Ivashchenko, Yuri  
; TITLE OF INVENTION: AKT NUCLEIC ACIDS, POLYPEPTIDES, AND USES THEREOF  
; FILE REFERENCE: A3278A-US  
; CURRENT APPLICATION NUMBER: US/09/526,043  
; CURRENT FILING DATE: 2000-03-14  
; EARLIER APPLICATION NUMBER: 60/125,108  
; EARLIER FILING DATE: 1999-03-19  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 14  
; LENGTH: 480  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-526-043-14

Query Match 99.8%; Score 2544; DB 10; Length 480;  
Best Local Similarity 99.8%; Pred. No. 6.7e-165;  
Matches 479; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 MSDVAIVKGEWLKRGGEYIKTRPRYFLKNDGTFIGYKERPDQVDQREAPLNPFSAQC 60  
Db 1 MSDVAIVKGEWLKRGGEYIKTRPRYFLKNDGTFIGYKERPDQVDQREAPLNPFSAQC 60  
Qy 61 QLMKTERPRNTFIIRCLQWTVIERTPHVETPEEREETTAIQTVDGLKKQEEEMDF 120  
Db 61 QLMKTERPRNTFIIRCLQWTVIERTPHVETPEEREETTAIQTVDGLKKQEEEMDF 120  
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Db 121 RSGSPSDNSGAEEMVSLAKPKHRTVMNEFYLLKLGKGTGKVLVKEKATGRYAMKI 180  
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Db 421 LSPFPKQVTSSETDTRYFDEEFTAQMITITPPDQDSDMECVDSERRRHPFQFSYSASGTA 480

APPLICANT: Takao Isogai  
APPLICANT: Tetsuo Nishikawa  
APPLICANT: Koji Hayaashi  
APPLICANT: Kaoru Otsuka  
APPLICANT: Jun-ichi Yamamoto  
APPLICANT: Shizuko Iehii  
APPLICANT: Tomoyasu Sugiyama  
APPLICANT: Ai Wakamatsu  
APPLICANT: Keiichi Nagai  
APPLICANT: Tetsuji Otsuki  
APPLICANT: Shin-ichi Funahashi  
APPLICANT: Chiaki Senoo  
APPLICANT: Jun-ichi Nezu  
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN KINASE/PROTEIN PHOSPHATASE  
FILE REFERENCE: 06501-099002  
CURRENT APPLICATION NUMBER: US/10/060,065  
PRIOR FILING DATE: 2002-01-29  
PRIOR APPLICATION NUMBER: PCT/JP00/05061  
PRIOR FILING DATE: 2000-07-28  
PRIOR APPLICATION NUMBER: US 60/159,590  
PRIOR FILING DATE: 1999-10-18  
PRIOR APPLICATION NUMBER: US 60/183,322  
PRIOR FILING DATE: 2000-02-17  
PRIOR APPLICATION NUMBER: JP 11-248036  
PRIOR FILING DATE: 1999-07-29  
PRIOR APPLICATION NUMBER: JP 2000-118776  
PRIOR FILING DATE: 2000-01-11  
PRIOR APPLICATION NUMBER: JP 2000-183767  
PRIOR FILING DATE: 2000-05-02  
PRIOR APPLICATION NUMBER: JP 2000-241899  
PRIOR FILING DATE: 2000-06-09  
NUMBER OF SEQ ID NOS: 43  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 18  
LENGTH: 480  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-060-065-18

Query Match 99.8%; Score 2544; DB 14; Length 480;  
Best Local Similarity 99.8%; Pred. No. 6.7e-165;  
Matches 479; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 MSDVAIVKEGWLKRGGEYIKTWPRYFLKNDGTFIGYKERPDVDQREAPLNFSVAQC 60  
Db 1 MSDVAIVKEGWLKRGGEYIKTWPRYFLKNDGTFIGYKERPDVDQREAPLNFSVAQC 60  
Qy 61 QLMKTERPRNTFIIRCLQWTTVIERTFHVETPEEREETTAIQTVADGLKKQEEEMDF 120  
Db 61 QLMKTERPRNTFIIRCLQWTTVIERTFHVETPEEREETTAIQTVADGLKKQEEEMDF 120  
Qy 121 RSGSPDSNGAEEMVSLAKPKHRVTWNEPEYLLKLGKTFGKVLVKEKATGRYYAMKI 180  
Db 121 RSGSPDSNGAEEMVSLAKPKHRVTWNEPEYLLKLGKTFGKVLVKEKATGRYYAMKI 180  
Qy 181 LKKEVIVAKDEVATHTLNRVQLNSRHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLS 240  
Db 181 LKKEVIVAKDEVATHTLNRVQLNSRHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLS 240  
Qy 241 RERVFSDDRARFYGAIEVSALDYLSHSEKNVYVRDLKLENMLDKDGHIKITDFGLCKEGI 300  
Db 241 RERVFSDDRARFYGAIEVSALDYLSHSEKNVYVRDLKLENMLDKDGHIKITDFGLCKEGI 300  
Qy 301 KDGATMTKTCGTPEYLAPEVLENDYGRADVWGLGVVVMEMCGRLPFYVNDHEKLPFEL 360  
Db 301 KDGATMTKTCGTPEYLAPEVLENDYGRADVWGLGVVVMEMCGRLPFYVNDHEKLPFEL 360  
Qy 361 ILMBEIRPRTLGPFAKSLLSGLLKKDKPKQLGGSEDAKEIMOHRRFAGIVWQHVYEXK 420  
Db 361 ILMBEIRPRTLGPFAKSLLSGLLKKDKPKQLGGSEDAKEIMOHRRFAGIVWQHVYEXK 420  
Qy 421 LSPFPKQVTSSETDTRYFDEEFTAQMITITPPDQDSDMECVDSERRRPHFPQFSYSASGTA 480  
Db 421 LSPFPKQVTSSETDTRYFDEEFTAQMITITPPDQDSDMECVDSERRRPHFPQFSYSASGTA 480

Db 421 LSPFPKQVTSSETDTRYFDEEFTAQMITITPPDQDSDMECVDSERRRPHFPQFSYSASSTA 480  
RESULT 7  
US-10-059-585-39  
Sequence 39, Application US/10059585  
Publication NO. US20030082776A1  
GENERAL INFORMATION:  
APPLICANT: Ota, Toshio  
APPLICANT: Isogai, Takao  
APPLICANT: Nishikawa, Tetsuo  
APPLICANT: Hayaashi, Koji  
APPLICANT: Otsuka, Kaoru  
APPLICANT: Yamamoto, Jun-ichi  
APPLICANT: Iehii, Shizuko  
APPLICANT: Sugiyama, Tomoyasu  
APPLICANT: Wakamatsu, Ai  
APPLICANT: Nagai, Keiichi  
APPLICANT: Otsuki, Tetsuji  
APPLICANT: Funahashi, Shin-ichi  
APPLICANT: Senoo, Chiaki  
APPLICANT: Nezu, Jun-ichi  
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN KINASE/PROTEIN PHOSPHATASE  
FILE REFERENCE: 06501-098001  
CURRENT APPLICATION NUMBER: US/10/059,585  
CURRENT FILING DATE: 2002-01-29  
PRIOR APPLICATION NUMBER: PCT/JP00/05060  
PRIOR FILING DATE: 2000-07-28  
PRIOR APPLICATION NUMBER: US 60/183,322  
PRIOR FILING DATE: 2000-02-17  
PRIOR APPLICATION NUMBER: US 60/159,590  
PRIOR FILING DATE: 1999-10-18  
PRIOR APPLICATION NUMBER: JP 2000-118776  
PRIOR FILING DATE: 2000-01-11  
PRIOR APPLICATION NUMBER: JP 2000-183767  
PRIOR FILING DATE: 2000-05-02  
PRIOR APPLICATION NUMBER: JP 11-248036  
PRIOR FILING DATE: 1999-07-29  
NUMBER OF SEQ ID NOS: 64  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 39  
LENGTH: 480  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-059-585-39

Query Match 99.8%; Score 2544; DB 14; Length 480;  
Best Local Similarity 99.8%; Pred. No. 6.7e-165;  
Matches 479; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 MSDVAIVKEGWLKRGGEYIKTWPRYFLKNDGTFIGYKERPDVDQREAPLNFSVAQC 60  
Db 1 MSDVAIVKEGWLKRGGEYIKTWPRYFLKNDGTFIGYKERPDVDQREAPLNFSVAQC 60  
Qy 61 QLMKTERPRNTFIIRCLQWTTVIERTFHVETPEEREETTAIQTVADGLKKQEEEMDF 120  
Db 61 QLMKTERPRNTFIIRCLQWTTVIERTFHVETPEEREETTAIQTVADGLKKQEEEMDF 120  
Qy 121 RSGSPDSNGAEEMVSLAKPKHRVTWNEPEYLLKLGKTFGKVLVKEKATGRYYAMKI 180  
Db 121 RSGSPDSNGAEEMVSLAKPKHRVTWNEPEYLLKLGKTFGKVLVKEKATGRYYAMKI 180  
Qy 181 LKKEVIVAKDEVATHTLNRVQLNSRHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLS 240  
Db 181 LKKEVIVAKDEVATHTLNRVQLNSRHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLS 240  
Qy 241 RERVFSDDRARFYGAIEVSALDYLSHSEKNVYVRDLKLENMLDKDGHIKITDFGLCKEGI 300  
Db 241 RERVFSDDRARFYGAIEVSALDYLSHSEKNVYVRDLKLENMLDKDGHIKITDFGLCKEGI 300  
Qy 301 KDGATMTKTCGTPEYLAPEVLENDYGRADVWGLGVVVMEMCGRLPFYVNDHEKLPFEL 360  
Db 301 KDGATMTKTCGTPEYLAPEVLENDYGRADVWGLGVVVMEMCGRLPFYVNDHEKLPFEL 360

Db 301 KGATMTKTCGTPEYLAPEVLENDYGRAVDWGLGVVYEMMCGRLPFYVQDHEKLFEL 360  
Qy 361 LMEEIRPRTLGPPEAKSLLSGLLKDPKQRLGGSEDAKEIMQHRFPAGIWHQVYVEKK 420  
Db 361 LMEEIRPRTLGPPEAKSLLSGLLKDPKQRLGGSEDAKEIMQHRFPAGIWHQVYVEKK 420  
Qy 421 LSPFPKQVTSSETDTRYDEFTAQMITITPPDODDSMECVDSERRRPHFPQFSYASGTA 480  
Db 421 LSPFPKQVTSSETDTRYDEFTAQMITITPPDODDSMECVDSERRRPHFPQFSYASGTA 480

RESULT 8  
US-10-394-322A-1  
; Sequence 1, Application US/10394322A  
; Publication No. US20030232391A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNESIS PHARMACEUTICALS, INC.  
; APPLICANT: Prescott, John C.  
; TITLE OF INVENTION: IDENTIFICATION OF KINASE INHIBITORS  
; FILE REFERENCE: 39750-0006 US  
; CURRENT APPLICATION NUMBER: US/10/394,322A  
; CURRENT FILING DATE: 2003-03-20  
; PRIOR FILING DATE: 2003-03-20  
; PRIOR FILING DATE: 2003-03-21  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 480  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-394-322A-1

Query Match 99.8%; Score 2544; DB 15; Length 480;  
Best Local Similarity 99.8%; Pred. No. 6.7e-165;  
Matches 479; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSDVAIVKEGWLHKGGEYIKTRPRYFLKNDGTFIGYKERPDVDQREAPLNNFSVAQC 60  
Db 1 MSDVAIVKEGWLHKGGEYIKTRPRYFLKNDGTFIGYKERPDVDQREAPLNNFSVAQC 60

Qy 61 QLMKTERPRNTFIIRCLQWTVIERTFHVETPEEREETTAIQTVDGLKKQEEEMDF 120  
Db 61 QLMKTERPRNTFIIRCLQWTVIERTFHVETPEEREETTAIQTVDGLKKQEEEMDF 120

Qy 121 RSGSPDSNGAEEMVSLAKPKRVTWNEFEYLLKLGKTFGKVLVKEKATGRYAMKI 180  
Db 121 RSGSPDSNGAEEMVSLAKPKRVTWNEFEYLLKLGKTFGKVLVKEKATGRYAMKI 180

Qy 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSPQTHDRLCFVMEYANGGELFFHLS 240  
Db 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSPQTHDRLCFVMEYANGGELFFHLS 240

Qy 241 RERVSEDRARFYGAIEVSALDYLHSEKNVYVRDLKLENMLDKDGHIKITDFGLCKEGI 300  
Db 241 RERVSEDRARFYGAIEVSALDYLHSEKNVYVRDLKLENMLDKDGHIKITDFGLCKEGI 300

Qy 301 KGATMTKTCGTPEYLAPEVLENDYGRAVDWGLGVVYEMMCGRLPFYVQDHEKLFEL 360  
Db 301 KGATMTKTCGTPEYLAPEVLENDYGRAVDWGLGVVYEMMCGRLPFYVQDHEKLFEL 360

Qy 361 LMEEIRPRTLGPPEAKSLLSGLLKDPKQRLGGSEDAKEIMQHRFPAGIWHQVYVEKK 420  
Db 361 LMEEIRPRTLGPPEAKSLLSGLLKDPKQRLGGSEDAKEIMQHRFPAGIWHQVYVEKK 420

Qy 421 LSPFPKQVTSSETDTRYDEFTAQMITITPPDODDSMECVDSERRRPHFPQFSYASGTA 480  
Db 421 LSPFPKQVTSSETDTRYDEFTAQMITITPPDODDSMECVDSERRRPHFPQFSYASGTA 480

RESULT 9  
US-10-217-574-31  
; Sequence 31, Application US/10217574  
; Publication No. US20040005687A1

; GENERAL INFORMATION:  
; APPLICANT: Barford, David  
; APPLICANT: Yang, Jing  
; APPLICANT: Hemmings, Brian A  
; APPLICANT: Cron, Peter D  
; TITLE OF INVENTION: Kinase Crystal Structures  
; FILE REFERENCE: 44237  
; CURRENT APPLICATION NUMBER: US/10/217,574  
; CURRENT FILING DATE: 2002-12-23  
; PRIOR FILING DATE: 2001-08-14  
; PRIOR FILING DATE: 2001-08-14  
; PRIOR FILING DATE: 2002-05-01  
; PRIOR FILING DATE: 2002-05-01  
; PRIOR FILING DATE: 2002-07-12  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 31  
; LENGTH: 480  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-217-574-31

Query Match 99.8%; Score 2544; DB 15; Length 480;  
Best Local Similarity 99.8%; Pred. No. 6.7e-165;  
Matches 479; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSDVAIVKEGWLHKGGEYIKTRPRYFLKNDGTFIGYKERPDVDQREAPLNNFSVAQC 60  
Db 1 MSDVAIVKEGWLHKGGEYIKTRPRYFLKNDGTFIGYKERPDVDQREAPLNNFSVAQC 60

Qy 61 QLMKTERPRNTFIIRCLQWTVIERTFHVETPEEREETTAIQTVDGLKKQEEEMDF 120  
Db 61 QLMKTERPRNTFIIRCLQWTVIERTFHVETPEEREETTAIQTVDGLKKQEEEMDF 120

Qy 121 RSGSPDSNGAEEMVSLAKPKRVTWNEFEYLLKLGKTFGKVLVKEKATGRYAMKI 180  
Db 121 RSGSPDSNGAEEMVSLAKPKRVTWNEFEYLLKLGKTFGKVLVKEKATGRYAMKI 180

Qy 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSPQTHDRLCFVMEYANGGELFFHLS 240  
Db 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSPQTHDRLCFVMEYANGGELFFHLS 240

Qy 241 RERVSEDRARFYGAIEVSALDYLHSEKNVYVRDLKLENMLDKDGHIKITDFGLCKEGI 300  
Db 241 RERVSEDRARFYGAIEVSALDYLHSEKNVYVRDLKLENMLDKDGHIKITDFGLCKEGI 300

Qy 301 KGATMTKTCGTPEYLAPEVLENDYGRAVDWGLGVVYEMMCGRLPFYVQDHEKLFEL 360  
Db 301 KGATMTKTCGTPEYLAPEVLENDYGRAVDWGLGVVYEMMCGRLPFYVQDHEKLFEL 360

Qy 361 LMEEIRPRTLGPPEAKSLLSGLLKDPKQRLGGSEDAKEIMQHRFPAGIWHQVYVEKK 420  
Db 361 LMEEIRPRTLGPPEAKSLLSGLLKDPKQRLGGSEDAKEIMQHRFPAGIWHQVYVEKK 420

Qy 421 LSPFPKQVTSSETDTRYDEFTAQMITITPPDODDSMECVDSERRRPHFPQFSYASGTA 480  
Db 421 LSPFPKQVTSSETDTRYDEFTAQMITITPPDODDSMECVDSERRRPHFPQFSYASGTA 480

RESULT 10  
US-10-217-555-31  
; Sequence 31, Application US/10217555  
; Publication No. US20040009569A1  
; GENERAL INFORMATION:  
; APPLICANT: Barford, David  
; APPLICANT: Hemmings, Brian A  
; APPLICANT: Cron, Peter D  
; TITLE OF INVENTION: Kinase Crystal Structures and Materials and Methods for  
; TITLE OF INVENTION: Kinase Activation  
; FILE REFERENCE: 44236  
; CURRENT APPLICATION NUMBER: US/10/217,555

```

; CURRENT FILING DATE: 2002-12-05
; PRIOR APPLICATION NUMBER: GB 0119860.5
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: GB 0209985.1
; PRIOR FILING DATE: 2002-05-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 31
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-217-555-31

Query Match          99.8%; Score 2544; DB 15; Length 480;
Best Local Similarity 99.8%; Pred. No. 6.7e-165;
Matches 479; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSDVAIVKEGWLHKGRIYKTRPRYFLKNDGTFIGYKRPQDVQDREAPLNFSVAQC 60
Db 1 MSDVAIVKEGWLHKGRIYKTRPRYFLKNDGTFIGYKRPQDVQDREAPLNFSVAQC 60

Qy 61 QLMKTERPRNTFIIRCLQWTTVIERTFHVETPEEREETTAIQTVDGLKKQEEEMDF 120
Db 61 QLMKTERPRNTFIIRCLQWTTVIERTFHVETPEEREETTAIQTVDGLKKQEEEMDF 120

Qy 121 RSGSPSDNSGAEEVSLAKPKHRTVMNEPEYLLKLGKTFGKVIIVKEKATGRYYAMKI 180
Db 121 RSGSPSDNSGAEEVSLAKPKHRTVMNEPEYLLKLGKTFGKVIIVKEKATGRYYAMKI 180

Qy 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMYANGGELPFHLS 240
Db 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMYANGGELPFHLS 240

Qy 241 RERVSEDRARFYGAIEVSALDYHSEKNVYVYRDLEMLDKDGHIKITDFGLCKEGI 300
Db 241 RERVSEDRARFYGAIEVSALDYHSEKNVYVYRDLEMLDKDGHIKITDFGLCKEGI 300

Qy 301 KDGATMKTFCGTPPYLAPEVLENDYGRAVDWGLGVVMYEMMCGRLPFYVQDHEKLFEL 360
Db 301 KDGATMKTFCGTPPYLAPEVLENDYGRAVDWGLGVVMYEMMCGRLPFYVQDHEKLFEL 360

Qy 361 LMEEIRFPRTLGPPEAKSLGSLKKDPKQRLGGSEDAKEIMQHRFFAGIVMHHVYEEK 420
Db 361 LMEEIRFPRTLGPPEAKSLGSLKKDPKQRLGGSEDAKEIMQHRFFAGIVMHHVYEEK 420

Qy 421 LSPFPKQVTSSETDTRFYDEEFTAQMITITPPDODDSMECVDSRRPFPQFSYSASGTA 480
Db 421 LSPFPKQVTSSETDTRFYDEEFTAQMITITPPDODDSMECVDSRRPFPQFSYSASGTA 480

RESULT 11
US-10-701-490-4
; Sequence 4, Application US/10701490
; Publication No. US20040106141A1
; GENERAL INFORMATION:
; APPLICANT: PAUL S. MISCHER
; APPLICANT: CHARLES L. SAWYERS
; APPLICANT: BRADLEY L. SMITH
; APPLICANT: KATHERINE CROSBY
; TITLE OF INVENTION: METHODS AND MATERIALS FOR EXAMINING
; FILE REFERENCE: GAC 30435.148USU1
; CURRENT APPLICATION NUMBER: US/10701490
; CURRENT FILING DATE: 2003-11-05
; PRIOR APPLICATION NUMBER: 60/423,777
; PRIOR FILING DATE: 2002-11-05
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-701-490-4

Query Match          99.8%; Score 2544; DB 16; Length 480;
Best Local Similarity 99.8%; Pred. No. 6.7e-165;
Matches 479; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSDVAIVKEGWLHKGRIYKTRPRYFLKNDGTFIGYKRPQDVQDREAPLNFSVAQC 60
Db 1 MSDVAIVKEGWLHKGRIYKTRPRYFLKNDGTFIGYKRPQDVQDREAPLNFSVAQC 60

Qy 61 QLMKTERPRNTFIIRCLQWTTVIERTFHVETPEEREETTAIQTVDGLKKQEEEMDF 120
Db 61 QLMKTERPRNTFIIRCLQWTTVIERTFHVETPEEREETTAIQTVDGLKKQEEEMDF 120

Qy 121 RSGSPSDNSGAEEVSLAKPKHRTVMNEPEYLLKLGKTFGKVIIVKEKATGRYYAMKI 180
Db 121 RSGSPSDNSGAEEVSLAKPKHRTVMNEPEYLLKLGKTFGKVIIVKEKATGRYYAMKI 180

Qy 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMYANGGELPFHLS 240
Db 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMYANGGELPFHLS 240

Qy 241 RERVSEDRARFYGAIEVSALDYHSEKNVYVYRDLEMLDKDGHIKITDFGLCKEGI 300
Db 241 RERVSEDRARFYGAIEVSALDYHSEKNVYVYRDLEMLDKDGHIKITDFGLCKEGI 300

Qy 301 KDGATMKTFCGTPPYLAPEVLENDYGRAVDWGLGVVMYEMMCGRLPFYVQDHEKLFEL 360
Db 301 KDGATMKTFCGTPPYLAPEVLENDYGRAVDWGLGVVMYEMMCGRLPFYVQDHEKLFEL 360

Qy 361 LMEEIRFPRTLGPPEAKSLGSLKKDPKQRLGGSEDAKEIMQHRFFAGIVMHHVYEEK 420
Db 361 LMEEIRFPRTLGPPEAKSLGSLKKDPKQRLGGSEDAKEIMQHRFFAGIVMHHVYEEK 420

Qy 421 LSPFPKQVTSSETDTRFYDEEFTAQMITITPPDODDSMECVDSRRPFPQFSYSASGTA 480
Db 421 LSPFPKQVTSSETDTRFYDEEFTAQMITITPPDODDSMECVDSRRPFPQFSYSASGTA 480

RESULT 12
US-10-713-678-2
; Sequence 2, Application US/10713678
; Publication No. US20040122077A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth Walsh
; APPLICANT: St. Elizabeth's Medical Center
; TITLE OF INVENTION: HMG CoA Reductase Inhibitors for
; FILE REFERENCE: 49,784 (1417)
; CURRENT APPLICATION NUMBER: US/10713,678
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: US/09/590,740
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-713-678-2

Query Match          99.8%; Score 2544; DB 16; Length 480;
Best Local Similarity 99.8%; Pred. No. 6.7e-165;
Matches 479; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSDVAIVKEGWLHKGRIYKTRPRYFLKNDGTFIGYKRPQDVQDREAPLNFSVAQC 60
Db 1 MSDVAIVKEGWLHKGRIYKTRPRYFLKNDGTFIGYKRPQDVQDREAPLNFSVAQC 60

Qy 61 QLMKTERPRNTFIIRCLQWTTVIERTFHVETPEEREETTAIQTVDGLKKQEEEMDF 120
Db 61 QLMKTERPRNTFIIRCLQWTTVIERTFHVETPEEREETTAIQTVDGLKKQEEEMDF 120

Qy 121 RSGSPSDNSGAEEVSLAKPKHRTVMNEPEYLLKLGKTFGKVIIVKEKATGRYYAMKI 180
Db 121 RSGSPSDNSGAEEVSLAKPKHRTVMNEPEYLLKLGKTFGKVIIVKEKATGRYYAMKI 180

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Db 121 RSGSPDSNGAEEMEVS LAKPKHRTWNEFYLKLGKTFGKVLVKEKATGRYYAMKI 180  
Qy 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLS 240  
Db 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLS 240  
Qy 241 RERVSEDRARFYGAETVSALDYLHSEKNVYVRDLKLENMLDKDGHIKITDFGLCKEGI 300  
Db 241 RERVSEDRARFYGAETVSALDYLHSEKNVYVRDLKLENMLDKDGHIKITDFGLCKEGI 300  
Qy 301 KDGATMTKTCGTPPYLAPEVLEDNDYGRAVDWGLGVVYEMWCGRLPFYFNQDHEKLFEL 360  
Db 301 KDGATMTKTCGTPPYLAPEVLEDNDYGRAVDWGLGVVYEMWCGRLPFYFNQDHEKLFEL 360  
Qy 361 ILMBEIRPRTLGPPEAKSLLSGLLKQPKORLGGGSEDAKIMQHRFPFAGIWMQHVYEEK 420  
Db 361 ILMBEIRPRTLGPPEAKSLLSGLLKQPKORLGGGSEDAKIMQHRFPFAGIWMQHVYEEK 420  
Qy 421 LSPFPKQVTSSETDTRYFDEEFTAQMITITPPDODDSMECVDSERRRPHFPQFSYSASGTA 480  
Db 421 LSPFPKQVTSSETDTRYFDEEFTAQMITITPPDODDSMECVDSERRRPHFPQFSYSASGTA 480

RESULT 13  
US-10-746-545-36  
; Sequence 36, Application US/10746545  
; Publication No. US20040171075A1  
; GENERAL INFORMATION:  
; APPLICANT: Deciphera Pharmaceuticals, Inc.  
; APPLICANT: Flynn, Daniel L.  
; APPLICANT: Petillo, Peter A.  
; TITLE OF INVENTION: MODULATION OF PROTEIN FUNCTIONALITIES  
; FILE REFERENCE: 34475  
; CURRENT APPLICATION NUMBER: US/10746.545  
; CURRENT FILING DATE: 2003-12-24  
; PRIOR APPLICATION NUMBER: US 60/437,487  
; PRIOR FILING DATE: 2002-12-31  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 36  
; LENGTH: 480  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-746-545-36

Query Match 99.8%; Score 2544; DB 16; Length 480;  
Best Local Similarity 99.8%; Pred. No. 6.7e-165;  
Matches 479; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSDVAIVKEGWLHKRGYIKTWPRPYFLKNDGTFIGYKERPDQVDDQREAPLNFSVAQC 60  
Db 1 MSDVAIVKEGWLHKRGYIKTWPRPYFLKNDGTFIGYKERPDQVDDQREAPLNFSVAQC 60  
Qy 61 QLMKTERPRNTFIIRCLQWTTVIERTFHVETPEEREETTAIQTVA DGLKKQEEEMDF 120  
Db 61 QLMKTERPRNTFIIRCLQWTTVIERTFHVETPEEREETTAIQTVA DGLKKQEEEMDF 120  
Qy 121 RSGSPDSNGAEEMEVS LAKPKHRTWNEFYLKLGKTFGKVLVKEKATGRYYAMKI 180  
Db 121 RSGSPDSNGAEEMEVS LAKPKHRTWNEFYLKLGKTFGKVLVKEKATGRYYAMKI 180  
Qy 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLS 240  
Db 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLS 240  
Qy 241 RERVSEDRARFYGAETVSALDYLHSEKNVYVRDLKLENMLDKDGHIKITDFGLCKEGI 300  
Db 241 RERVSEDRARFYGAETVSALDYLHSEKNVYVRDLKLENMLDKDGHIKITDFGLCKEGI 300  
Qy 301 KDGATMTKTCGTPPYLAPEVLEDNDYGRAVDWGLGVVYEMWCGRLPFYFNQDHEKLFEL 360  
Db 301 KDGATMTKTCGTPPYLAPEVLEDNDYGRAVDWGLGVVYEMWCGRLPFYFNQDHEKLFEL 360

Qy 361 ILMBEIRPRTLGPPEAKSLLSGLLKQPKORLGGGSEDAKIMQHRFPFAGIWMQHVYEEK 420  
Db 361 ILMBEIRPRTLGPPEAKSLLSGLLKQPKORLGGGSEDAKIMQHRFPFAGIWMQHVYEEK 420  
Qy 421 LSPFPKQVTSSETDTRYFDEEFTAQMITITPPDODDSMECVDSERRRPHFPQFSYSASGTA 480  
Db 421 LSPFPKQVTSSETDTRYFDEEFTAQMITITPPDODDSMECVDSERRRPHFPQFSYSASGTA 480

RESULT 14  
US-10-103-256-11  
; Sequence 11, Application US/10103256  
; Publication No. US20030181366A1  
; GENERAL INFORMATION:  
; APPLICANT: Abbott Laboratories  
; APPLICANT: Luo, Yan  
; APPLICANT: Giranda, Vincent L.  
; APPLICANT: Smith, Richard A.  
; APPLICANT: Richardson, Paul L.  
; APPLICANT: Hutchins, Charles  
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF AKT AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: 6904.US.O1  
; CURRENT APPLICATION NUMBER: US/10/103.256  
; CURRENT FILING DATE: 2002-07-09  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11  
; LENGTH: 524  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-103-256-11

Query Match 99.8%; Score 2544; DB 14; Length 524;  
Best Local Similarity 99.8%; Pred. No. 7.4e-165;  
Matches 479; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSDVAIVKEGWLHKRGYIKTWPRPYFLKNDGTFIGYKERPDQVDDQREAPLNFSVAQC 60  
Db 45 MSDVAIVKEGWLHKRGYIKTWPRPYFLKNDGTFIGYKERPDQVDDQREAPLNFSVAQC 104  
Qy 61 QLMKTERPRNTFIIRCLQWTTVIERTFHVETPEEREETTAIQTVA DGLKKQEEEMDF 120  
Db 105 QLMKTERPRNTFIIRCLQWTTVIERTFHVETPEEREETTAIQTVA DGLKKQEEEMDF 164  
Qy 121 RSGSPDSNGAEEMEVS LAKPKHRTWNEFYLKLGKTFGKVLVKEKATGRYYAMKI 180  
Db 165 RSGSPDSNGAEEMEVS LAKPKHRTWNEFYLKLGKTFGKVLVKEKATGRYYAMKI 224  
Qy 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLS 240  
Db 225 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLS 284  
Qy 241 RERVSEDRARFYGAETVSALDYLHSEKNVYVRDLKLENMLDKDGHIKITDFGLCKEGI 300  
Db 285 RERVSEDRARFYGAETVSALDYLHSEKNVYVRDLKLENMLDKDGHIKITDFGLCKEGI 344  
Qy 301 KDGATMTKTCGTPPYLAPEVLEDNDYGRAVDWGLGVVYEMWCGRLPFYFNQDHEKLFEL 360  
Db 345 KDGATMTKTCGTPPYLAPEVLEDNDYGRAVDWGLGVVYEMWCGRLPFYFNQDHEKLFEL 404  
Qy 361 ILMBEIRPRTLGPPEAKSLLSGLLKQPKORLGGGSEDAKIMQHRFPFAGIWMQHVYEEK 420  
Db 405 ILMBEIRPRTLGPPEAKSLLSGLLKQPKORLGGGSEDAKIMQHRFPFAGIWMQHVYEEK 464  
Qy 421 LSPFPKQVTSSETDTRYFDEEFTAQMITITPPDODDSMECVDSERRRPHFPQFSYSASGTA 480  
Db 465 LSPFPKQVTSSETDTRYFDEEFTAQMITITPPDODDSMECVDSERRRPHFPQFSYSASGTA 524

RESULT 15  
US-10-365-348-11

; Sequence 11, Application US/10365348  
; Publication No. US20040038883A1  
; GENERAL INFORMATION:  
; APPLICANT: Abbott Laboratories  
; APPLICANT: Luo, Yan  
; APPLICANT: Giranda, Vincent L.  
; APPLICANT: Richardson, Paul L.  
; APPLICANT: Smith, Richard A.  
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF AKT AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: 6904 US P1  
; CURRENT APPLICATION NUMBER: US/10/365,348  
; CURRENT FILING DATE: 2003-02-12  
; PRIOR APPLICATION NUMBER: 10/103,256  
; PRIOR FILING DATE: 2002-03-21  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11  
; LENGTH: 524  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-365-348-11

Query Match 99.8%; Score 2544; DB 15; Length 524;  
Best Local Similarity 99.8%; Pred. No. 7.4e-165;  
Matches 479; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 1 MSDVAIVKEGWLKRGVEIKTWPRYFLKNDGTFIGYKERPDVDQREAPLNNFSVAQC 60  
Db |||||  
Qy 45 MSDVAIVKEGWLKRGVEIKTWPRYFLKNDGTFIGYKERPDVDQREAPLNNFSVAQC 104  
Db |||||  
Qy 61 QLMKTERPRNTFIIRCLQWTVIERTFHVETPEERESEWTTAIQTVDAGLKKQEEEMDF 120  
Db |||||  
Qy 105 QLMKTERPRNTFIIRCLQWTVIERTFHVETPEERESEWTTAIQTVDAGLKKQEEEMDF 164  
Db |||||  
Qy 121 RSGSPSDNSGAEEMEVSIAKPKHRVTWNEPEYLLKLGKTFGKVLVKEKATGRYYAMKI 180  
Db |||||  
Qy 165 RSGSPSDNSGAEEMEVSIAKPKHRVTWNEPEYLLKLGKTFGKVLVKEKATGRYYAMKI 224  
Db |||||  
Qy 181 LKKEVIVAKDRVAHTLTENRVLQNSRHPFLTALAKYSFQTHDRLCFVMEYANGGELFFHLS 240  
Db |||||  
Qy 225 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALAKYSFQTHDRLCFVMEYANGGELFFHLS 284  
Db |||||  
Qy 241 RRVFSEDRARFYGAIEVSALDYLHSEKNVYRDLENLMLDKDGHIKITDFGLCKEGI 300  
Db |||||  
Qy 285 RRVFSEDRARFYGAIEVSALDYLHSEKNVYRDLENLMLDKDGHIKITDFGLCKEGI 344  
Db |||||  
Qy 301 KDGATMTKTCGTPPYLAPEVLENDYGRAVDWGLGVVYEMMCGRLPFYNDQHEKLFEL 360  
Db |||||  
Qy 345 KDGATMTKTCGTPPYLAPEVLENDYGRAVDWGLGVVYEMMCGRLPFYNDQHEKLFEL 404  
Db |||||  
Qy 361 LMEEIRPRTLGPPEAKSLGLKDPKORLGGSEDAKEIMOHRRFPAGIVMOHVYEKK 420  
Db |||||  
Qy 405 LMEEIRPRTLGPPEAKSLGLKDPKORLGGSEDAKEIMOHRRFPAGIVMOHVYEKK 464  
Db |||||  
Qy 421 LSPPFKQVTSSETDTRYFDEEFTAQMITITPPDODDSMECVDSERRPHFPQFSYASGTA 480  
Db |||||  
Qy 465 LSPPFKQVTSSETDTRYFDEEFTAQMITITPPDODDSMECVDSERRPHFPQFSYASSTA 524  
Db |||||

Search completed: February 23, 2005, 21:00:58  
Job time : 134 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model  
Run on: February 23, 2005, 20:23:28 ; Search time 174 Seconds  
(without alignments)  
1412.632 Million cell updates/sec

Title: US-10-621-485A-1  
Perfect score: 2550  
Sequence: 1 MSDVAIVKEGLHKGVEIK.....VDSERRPHFPQFSASGTA 480

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2550	100.0	480	Q9BWB6	Q9BWB6 homo sapien
2	2544	99.8	480	KRAC_HUMAN	P31749 homo sapien
3	2509	98.4	501	KAKT_MLVAT	P31748 akt8 murine
4	2507	98.3	480	KRAC_RAT	P47196 rattus norv
5	2503	98.2	480	KRAC_MOUSE	P31750 mus musculus
6	2464	96.6	480	O57513	O57513 gallus gall
7	2452	96.2	480	KRAC_BOVIN	Q01314 bos taurus
8	2378.5	93.3	481	Q98TY9	Q98TY9 xenopus lae
9	2303	90.3	452	Q8BS26	Q8BS26 mus musculus
10	2128.5	83.5	481	AKT2_MOUSE	Q60823 mus musculus
11	2126.5	83.4	481	AKT2_HUMAN	P31751 homo sapien
12	2119	83.1	486	Q72X15	Q72X15 xenopus lae
13	2113.5	82.9	481	AKT2_RAT	P47197 rattus norv
14	2105.5	82.6	479	AKT3_HUMAN	Q9Y243 homo sapien
15	2103.5	82.5	485	Q61P76	Q61P76 xenopus lae
16	2102.5	82.5	479	Q6NXW0	Q6NXW0 mus musculus
17	2097.5	82.3	479	AKT3_MOUSE	Q9WUA6 mus musculus
18	2066.5	81.0	479	Q8UUK0	Q8UUK0 brachydanio
19	1989.5	78.0	454	AKT3_RAT	Q63484 rattus norv
20	1988	78.0	478	Q802Y3	Q802Y3 brachydanio
21	1640.5	64.3	528	Q868D7	Q868D7 aedes aegypt
22	1615	63.3	571	Q7QK56	Q7QK56 anopheles g
23	1607.5	63.0	486	Q95YJ0	Q95YJ0 asterina pe
24	1595.5	62.6	353	Q8CE74	Q8CE74 mus musculus
25	1582.5	62.1	530	Q24293	Q24293 drosophila
26	1581.5	62.0	530	Q24469	Q24469 drosophila
27	1581.5	62.0	611	Q8INB9	Q8INB9 drosophila
28	1581.5	62.0	611	Q7JN11	Q7JN11 drosophila
29	1490.5	58.5	546	Q17942	Q17942 caenorhabdi
30	1470	57.6	541	Q17941	Q17941 caenorhabdi
31	1390.5	54.5	528	Q9XTG7	Q9XTG7 caenorhabdi

RESULT 1									
Q9BWB6	PRELIMINARY; PRT; 480 AA.								
ID	Q9BWB6;								
AC	Q9BWB6;								
DT	01-JUN-2001	(Tremblrel. 17, Created)							
DT	01-JUN-2001	(Tremblrel. 17, Last sequence update)							
DT	01-OCT-2003	(Tremblrel. 25, Last annotation update)							
DE	AKT1 protein.								
OS	Homo sapiens (Human).								
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.								
OX	NCBI_TaxID=9606;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RC	TISSUE=Muscle;								
RX	MEDLINE=23288257; PubMed=12477932; DOI=10.1073/pnas.242603899;								
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Diatchenko L., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C., Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalobon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smalilus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;								
RT	"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";								
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).								
RN	[2]								
RP	SEQUENCE FROM N.A.								
RC	TISSUE=Muscle;								
RA	Strausberg R.;								
RL	Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.								
CC	-1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.								
CC	-1- SIMILARITY: Contains 1 PH domain.								
DR	EMBL; BC000479; AA00479.1; -								
DR	HSSP; P31749; 1H10.								
DR	GO; GO:0005524; F:ATP binding; IEA.								
DR	GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.								
DR	GO; GO:0016740; F:transferase activity; IEA.								
DR	GO; GO:0006468; P:protein amino acid phosphorylation; IEA.								
DR	InterPro; IPR011009; Kinase_like.								
DR	InterPro; IPR001849; PH.								
DR	InterPro; IPR011036; PH_related.								
DR	InterPro; IPR000961; Pkinase_C.								
DR	InterPro; IPR000719; Prot_kinase.								

## ALIGNMENTS

32	1324	51.9	483	2	Q77145	O77145 caenorhabdi
33	1317	51.6	387	2	Q8MUAS	Q8MUAS hydra atten
34	1108.5	43.5	246	2	Q9PUJ3	Q9PUJ3 gallus gall
35	1087	42.6	201	2	Q9BV07	Q9BV07 homo sapien
36	953	37.4	286	2	Q66XT6	Q66XT6 anopheles s
37	938	36.8	444	1	KRAC_DICDI	P54644 dictyosteli
38	901	35.3	198	2	Q8C6X4	Q8C6X4 mus musculus
39	895	35.1	466	2	Q761W9	Q761W9 encamoeba h
40	874.5	34.3	427	1	SGK2_HUMAN	Q9HBY8 homo sapien
41	862	33.8	432	2	Q6U1I9	Q6U1I9 gallus gall
42	860.5	33.7	519	2	Q6NS85	Q6NS85 mus musculus
43	856	33.6	687	2	Q6GNZ7	Q6GNZ7 xenopus lae
44	855	33.5	671	1	KPCB_HUMAN	P05771 homo sapien
45	855	33.5	671	1	KPCB_MOUSE	P04410 mus musculus

```

DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF00169; PH; 1.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF00433; Pkinase_C; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00233; PH; 1.
DR SMART; SM00220; S_TK; 1.
DR SMART; SM00133; S_TK_X; 1.
DR PROSITE; PS00003; PH DOMAIN; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 480 AA; 55686 MW; 6EAF4F8AD436714 CRC64;

Query March 100.0%; Score 2550; DB 2; Length 480;
Best Local Similarity 100.0%; Pred. No. 1.4e-152;
Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSDVAIVKEGLHKGGEYIKTWPRYFLKNDGTFIGYKERPDVDQREAPLNFSVAQC 60
Db 1 MSDVAIVKEGLHKGGEYIKTWPRYFLKNDGTFIGYKERPDVDQREAPLNFSVAQC 60

Qy 61 QLMKTERPRNPTFIIRCLQWTVIERTFHVETPEEREETWTAIQTVADGLKKQEEEMDF 120
Db 61 QLMKTERPRNPTFIIRCLQWTVIERTFHVETPEEREETWTAIQTVADGLKKQEEEMDF 120

Qy 121 RSGSPDSNGAEVEVSLAKPKHRTVNEFYLLKLGKTFGKVLVKEKATGRYYAMKI 180
Db 121 RSGSPDSNGAEVEVSLAKPKHRTVNEFYLLKLGKTFGKVLVKEKATGRYYAMKI 180

Qy 181 LKKEVIVAKDQVANTLTENRVLQNSRHPFLTALXVSFQTHDRLCFVMEYANGGLFFHLS 240
Db 181 LKKEVIVAKDQVANTLTENRVLQNSRHPFLTALXVSFQTHDRLCFVMEYANGGLFFHLS 240

Qy 241 RERFSEDRARFYGAIEVSALDYLHSEKNVYVRDLKLENLMLDKDGHIKITDFGLCKEGI 300
Db 241 RERFSEDRARFYGAIEVSALDYLHSEKNVYVRDLKLENLMLDKDGHIKITDFGLCKEGI 300

Qy 301 KOGATMTFCGTPPYLAPEVLVDNDYGRADVWNGLGVMYBMMCGRLPFYNQDHEKLFEL 360
Db 301 KOGATMTFCGTPPYLAPEVLVDNDYGRADVWNGLGVMYBMMCGRLPFYNQDHEKLFEL 360

Qy 361 ILMEIIRFRTLGPGLKSLGLKXPKQRLGGSDAKEMOHRFFAGLVQHVYVEKK 420
Db 361 ILMEIIRFRTLGPGLKSLGLKXPKQRLGGSDAKEMOHRFFAGLVQHVYVEKK 420

Qy 421 LSPFPKQVTSSETDTRYPDEFTAQMITITPPDQDDSMCVDSRRRPHFPQFSYASGTA 480
Db 421 LSPFPKQVTSSETDTRYPDEFTAQMITITPPDQDDSMCVDSRRRPHFPQFSYASGTA 480

RESULT 2
ID -KAC HUMAN STANDARD; PRT; 480 AA.
AC P31749;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE RAC-alpha serine/threonine-protein kinase (EC 2.7.1.37) (RAC-PK-alpha)
DE (Protein kinase B) (PKB) (C-AKT).
GN Name=AKT1; Synonyms=PKB, RAC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91239529; PubMed=1851997;
RA Jones P.F., Jakubowicz T., Picossi F.J., Maurer F., Hemmings B.A.;
RT "Molecular cloning and identification of a serine/threonine protein
RT kinase of the second-messenger subfamily.";

```

```

RL Proc. Natl. Acad. Sci. U.S.A. 88:4171-4175(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21399046; PubMed=11508278;
RA Matsubara A., Wasson J.C., Donelan S.S., Welling C.M., Glaser B.,
RA Permutt M.A.;
RT "Isolation and characterization of the human AKT1 gene, identification
RT of 13 single nucleotide polymorphisms (SNPs), and their lack of
RT association with Type II diabetes.";
RL Diabetologia 44:910-913(2001).
RN [3]
RP SEQUENCE OF 63-480 FROM N.A.
RC TISSUE=Forebrain;
RX MEDLINE=92037600; PubMed=1718748;
RA Coffey P.J., Woodgett J.R.;
RT "Molecular cloning and characterisation of a novel putative protein-
RT serine kinase related to the cAMP-dependent and protein kinase C
RT families.";
RL Eur. J. Biochem. 201:475-481(1991).
RN [4]
RP REVISIONS.
RX MEDLINE=92249329; PubMed=1533586;
RA Coffey P.J., Woodgett J.R.;
RL Eur. J. Biochem. 205:1217-1218(1992).
RN [5]
RP CHARACTERIZATION.
RX MEDLINE=98409636; PubMed=9736715; DOI=10.1073/pnas.95.19.11211;
RA Delcommenne M., Tan C., Gray V., Rue L., Woodgett J.R., Dedhar S.;
RT "Phosphoinositide-3-OH kinase-dependent regulation of glycogen
RT synthase kinase 3 and protein kinase B/AKT by the integrin-linked
RT kinase.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:11211-11216(1998).
RN [6]
RP MUTAGENESIS OF THR-308 AND SER-473, AND PHOSPHORYLATION SITES THR-308
RP AND SER-473.
RX MEDLINE=97133284; PubMed=8978681;
RA Alessi D.R., Andjelkovic M., Caudwell F.B., Cron P., Morrice N.,
RA Cohen P., Hemmings B.A.;
RT "Mechanism of activation of protein kinase B by insulin and IGF-1.";
RL EMBO J. 15:6541-6551(1996).
RN [7]
RP PHOSPHORYLATION SITE TYR-474, AND MUTAGENESIS OF TYR-474.
RX MEDLINE=92254844; PubMed=12142449; DOI=10.1074/jbc.M203387200;
RA Conus N.M., Hannan K.M., Cristiano B.E., Hemmings B.A., Pearson R.B.;
RT "Direct identification of tyrosine 474 as a regulatory phosphorylation
RT site for the Akt protein kinase.";
RL J. Biol. Chem. 277:38021-38028(2002).
CC -1- FUNCTION: General protein kinase capable of phosphorylating
CC several known proteins.
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphorylated protein.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic and nuclear after activation by
CC integrin-linked protein kinase 1 (ILK1).
CC -1- TISSUE SPECIFICITY: In all human cell types so far analyzed.
CC -1- DOMAIN: Binding of the PH domain to the phosphatidylinositol 3-
CC kinase alpha (PI(3)K) results in its targeting to the plasma
CC membrane.
CC -1- PTM: Phosphorylation on Thr-308, Ser-473 and Tyr-474 is required
CC for full activity.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. RAC
CC subfamily.
CC -1- SIMILARITY: Contains 1 PH domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M63167; AAA36539.1; -.
CC EMBL; AF283830; AAL55732.1; -.
CC EMBL; AF283819; AAL55732.1; JOINED.

```

DR EMBL; AF283820; AAL55732.1; JOINED.  
 DR EMBL; AF283821; AAL55732.1; JOINED.  
 DR EMBL; AF283822; AAL55732.1; JOINED.  
 DR EMBL; AF283823; AAL55732.1; JOINED.  
 DR EMBL; AF283824; AAL55732.1; JOINED.  
 DR EMBL; AF283825; AAL55732.1; JOINED.  
 DR EMBL; AF283826; AAL55732.1; JOINED.  
 DR EMBL; AF283827; AAL55732.1; JOINED.  
 DR EMBL; AF283828; AAL55732.1; JOINED.  
 DR EMBL; AF283829; AAL55732.1; JOINED.  
 DR EMBL; X61037; CAA43372.1; -.  
 DR PIR; A39360; A39360.  
 DR PDB; 1H10; X-ray; A=1-123.  
 DR InterAct; P31749; -.  
 DR Genew; HGNC:591; AKT1.  
 DR H-InvDB; HIX0012019; -.  
 DR MIM; 164730; -.  
 DR GO; GO:0004674; P:protein serine/threonine kinase activity; TAS.  
 DR GO; GO:0006916; P:anti-apoptosis; TAS.  
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; TAS.  
 DR GO; GO:0006809; P:nitric oxide biosynthesis; TAS.  
 DR GO; GO:0006464; P:protein modification; TAS.  
 DR GO; GO:0009408; P:response to heat; TAS.  
 DR GO; GO:0007165; P:signal transduction; TAS.  
 DR InterPro; IPR011009; Kinase\_like.  
 DR InterPro; IPR001849; PH\_related.  
 DR InterPro; IPR01036; PH\_related.  
 DR InterPro; IPR000961; Pkinase\_C.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
 DR InterPro; IPR002290; Ser\_thr\_pkinase.  
 DR Pfam; PF00169; PH; 1.  
 DR Pfam; PF00069; Pkinase; 1.  
 DR Pfam; PF00433; Pkinase\_C; 1.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR SMART; SM00233; PH; 1.  
 DR SMART; SM00133; S\_TK\_X; 1.  
 DR SMART; SM00220; S\_TK; 1.  
 DR PROSITE; PS50003; PH DOMAIN; 1.  
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
 DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 KW 3D-structure; ATP-binding; Nuclear protein; Phosphorylation;  
 KW Serine/threonine-protein kinase; Transferase.  
 FT DOMAIN 5 108 PH.  
 FT DOMAIN 150 408 Protein kinase.  
 FT NP\_BIND 156 164 ATP (By similarity).  
 FT BINDING 179 179 ATP (By similarity).  
 FT ACT\_SITE 274 274 Proton acceptor (By similarity).  
 FT MOD\_RES 308 308 Phosphothreonine (by PDK1).  
 FT MOD\_RES 473 473 Phosphoserine (by ILK1).  
 FT MOD\_RES 474 474 Phosphotyrosine.  
 FT MUTAGEN 308 308 T->D: 5-fold activation and 18-fold activation; when associated with D-473.  
 FT MUTAGEN 473 473 S->D: 7-fold activation and 25-fold activation; when associated with D-308.  
 FT MUTAGEN 474 474 Y->F: 55% inhibition of activation.  
 FT CONFLICT 173 174 L -> Q (in Ref. 3).  
 FT CONFLICT 202 202 L -> Q (in Ref. 3).  
 FT CONFLICT 212 212 A -> R (in Ref. 3).  
 FT CONFLICT 246 246 S -> A (in Ref. 3).  
 FT CONFLICT 409 409 A -> T (in Ref. 3).  
 FT CONFLICT 476 476 A -> P (in Ref. 3).  
 FT CONFLICT 478 478 S -> A (in Ref. 3).  
 SQ SEQUENCE 480 AA; 55716 MW; 6EAFE938AD436714 CRC64;  
 Query Match 99.8%; Score 2544; DB 1; Length 480;  
 Best Local Similarity 99.8%; Pred. No. 3.4e-152;  
 Matches 479; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 1 MSDVAIVKGEMLHKKRGEYIKTRPRYFLKNDGTGFIGYKRPQDDVDQREAPLNPFVSAQC 60  
 1 MSDVAIVKGEMLHKKRGEYIKTRPRYFLKNDGTGFIGYKRPQDDVDQREAPLNPFVSAQC 60

QY 61 QLMKTERPRNTFIIRCLQWTTVIERTPHVETPEREWTTAIQTVADGLKKQBESEMDF 120  
 DB 61 QLMKTERPRNTFIIRCLQWTTVIERTPHVETPEREWTTAIQTVADGLKKQBESEMDF 120  
 QY 121 RSGSPSDNSGAEEMEVSIAKPKHRTVWNEFYLLKLGKGTGKVLVKEKATGRYYAMKI 180  
 DB 121 RSGSPSDNSGAEEMEVSIAKPKHRTVWNEFYLLKLGKGTGKVLVKEKATGRYYAMKI 180  
 QY 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLS 240  
 DB 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLS 240  
 QY 241 RRVFSEDRARFYGAEIVSALDYHSEKNVYRDLKLENMLDKDGHIKITDFGLCKEGI 300  
 DB 241 RRVFSEDRARFYGAEIVSALDYHSEKNVYRDLKLENMLDKDGHIKITDFGLCKEGI 300  
 QY 301 KDGATMTKTCGTPEYLAPEVLEDNDYGRAVDWGLGVVYEMVCMGRLPFYNQDHEKLFEL 360  
 DB 301 KDGATMTKTCGTPEYLAPEVLEDNDYGRAVDWGLGVVYEMVCMGRLPFYNQDHEKLFEL 360  
 QY 361 ILMEEIFRPRTLGPPEAKSLGLLKQDKQRLGGSEDAKEIMQHRFFAGIVMQHVYKK 420  
 DB 361 ILMEEIFRPRTLGPPEAKSLGLLKQDKQRLGGSEDAKEIMQHRFFAGIVMQHVYKK 420  
 QY 421 LSPPEKQVTSSETDTRYFDEEFTAQMITITPPDODDSMECVDSERRPHPPQFSYSASCTA 480  
 DB 421 LSPPEKQVTSSETDTRYFDEEFTAQMITITPPDODDSMECVDSERRPHPPQFSYSASCTA 480

RESULT 3  
 KAKT\_MLVAT  
 ID KAKT\_MLVAT STANDARD; PRT; 501 AA.  
 AC P31748;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE AKT kinase transforming protein (EC 2.7.1.-).  
 GN Name=V-AKT;  
 OS AKT8 murine leukemia virus.  
 OC Viruses; Retroviral viruses; Retroviridae; Gammaretrovirus.  
 OX NCBI\_TaxID=11790;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92022574; PubMed=1833819;  
 RA Bellacosa A., Teeta J.R., Staal S.P., Tsichlis P.N.;  
 RT "A retroviral oncogene, akt, encoding a serine-threonine kinase  
 containing an SH2-like region.";  
 RL Science 254:274-277(1991).  
 CC -!- PTM: Autophosphorylated on threonine and serine residues.  
 CC -!- MISCELLANEOUS: This protein is synthesized as a Gag-Akt  
 polyprotein.  
 CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. RAC  
 subfamily.  
 CC -!- SIMILARITY: Contains 1 PH domain.  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 DR EMBL; M80675; AAA42545.1; -.  
 DR HSSP; P31749; 1H10.  
 DR InterPro; IPR011009; Kinase\_like.  
 DR InterPro; IPR001849; PH.  
 DR InterPro; IPR01036; PH\_related.  
 DR InterPro; IPR000961; Pkinase\_C.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
 DR InterPro; IPR002290; Ser\_thr\_pkinase.

```
DR Pfam; PF00169; PH; 1.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF00433; Pkinase; C; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00233; PH; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TK; 1.
DR PROSITE; PS00003; PH DOMAIN; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE_ST; 1.
DR PROSITE; PS00108; Oncogene; Phosphorylation;
KW Serine/threonine-protein kinase; Transferrase.
FT DOMAIN 26 129
FT DOMAIN 171 429
FT NP_BIND 177 185
FT BINDING 200 200
FT ACT_SITE 295 295
FT MOD_RES 347 347
SQ SEQUENCE 501 AA; 57870 MW; 5AEFDE58CD42F773 CRC64;

Query Match 98.4%; Score 2509; DB 1; Length 501;
Best Local Similarity 98.3%; Pred. No. 5.7e-150;
Matches 472; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MSDVAIVKEGWLHKGGEYIKTRPRYFLKNDGTFIGYKERPDVDQREAPLNFSVAQC 60
Db 22 MNDVAIVKEGWLHKGGEYIKTRPRYFLKNDGTFIGYKERPDVDQREAPLNFSVAQC 81
Qy 61 QLMKTERPRNPTFIIRCLQWTVIERTFHVETPEEREEWTTAIQTVDGLKKQEEEMDF 120
Db 82 QLMKTERPRNPTFIIRCLQWTVIERTFHVETPEEREEWTTAIQTVDGLKKQEEEMDF 141
Qy 121 RSGSPDSNGAEVEVSLAKPKHRTVWNEPFLYKLGKTFGKVLVKEKATGRYYAMKI 180
Db 142 RSGSPDSNGAEVEVSLAKPKHRTVWNEPFLYKLGKTFGKVLVKEKATGRYYAMKI 201
Qy 181 LKKEVIVAKDVAHTLFTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLS 240
Db 202 LKKEVIVAKDVAHTLFTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLS 261
Qy 241 RERFVEDRFRFYGAIEVSALDYLSHSEKNVYVYRDLKLENMLDKDGHKIKITDFGLCKEGI 300
Db 262 RERFVEDRFRFYGAIEVSALDYLSHSEKNVYVYRDLKLENMLDKDGHKIKITDFGLCKEGI 321
Qy 301 KOGATMTKTCFTPEYLAPEVLEDNDYGRAVDWGLGVVVMYEMWCGRLPFYNDQHEKLFEL 360
Db 322 KOGATMTKTCFTPEYLAPEVLEDNDYGRAVDWGLGVVVMYEMWCGRLPFYNDQHEKLFEL 381
Qy 361 ILMBEIRFPRTLGLPEAKSLLSGLLKQDPKQRLGGSGEDAKEIMQHRFFAGIVWQHVYEKK 420
Db 382 ILMBEIRFPRTLGLPEAKSLLSGLLKQDPQRLGGSGEDAKEIMQHRFFANIVWQDVYEKK 441
Qy 421 LSPFPKQVTSSETDTRVDFEFTAQMITITPPDQDDSMCEVDSRRRPHFPQFSYASGTA 480
Db 442 LSPFPKQVTSSETDTRVDFEFTAQMITITPPDQDDSMCEVDSRRRPHFPQFSYASGTA 501
```

## RESULT 4

```
KRAC RAT
ID KRAC RAT STANDARD; PRT; 480 AA.
AC P47196;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE RAC-alpha serine/threonine-protein kinase (EC 2.7.1.37) (RAC-PK-alpha)
DE (Protein kinase B) (PKB).
GN Name=Akt1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_taxid=10116;
RN [1]
```

```
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=95091823; PubMed=7999118;
RA Konishi H., Shinomura T., Kuroda S.I., Ono Y., Kikkawa U.;
RT "Molecular cloning of rat RAC protein kinase alpha and beta and their
RL Biochem. Biophys. Res. Commun. 205:817-825(1994).
CC -1- FUNCTION: General protein kinase capable of phosphorylating
CC several known proteins.
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic and nuclear after activation by
CC integrin-linked protein kinase 1 (ILK1) (By similarity).
CC -1- TISSUE SPECIFICITY: Widely expressed. Low levels found in liver
CC with slightly higher levels present in thymus and testis.
CC -1- DOMAIN: Binding of the PH domain to the phosphatidylinositol 3-
CC kinase alpha (PI(3)K) results in its targeting to the plasma
CC membrane.
CC -1- PTM: Phosphorylation on Thr-308, Ser-473 and Tyr-474 is required
CC for full activity.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. RAC
CC subfamily.
CC -1- SIMILARITY: Contains 1 PH domain.
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CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; D30040; BAA06279.1; -.
DR PIR; JC2437; JC2437.
DR HSP; P31749; IH10.
DR RGD; 2081; Akt1.
DR InterPro; IPR011009; Kinase_like.
DR InterPro; IPR001849; PH.
DR InterPro; IPR011036; PH related.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00169; PH; 1.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF00433; Pkinase_C; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00233; PH; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TK; 1.
DR PROSITE; PS00003; PH DOMAIN; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE_ST; 1.
KW ATP-binding; Phosphorylation; Serine/threonine-protein kinase;
KW Transferrase.
FT DOMAIN 5 108
FT DOMAIN 150 408
FT NP_BIND 156 164
FT BINDING 179 179
FT ACT_SITE 274 274
FT MOD_RES 308 308
FT MOD_RES 473 473
FT MOD_RES 474 474
SQ SEQUENCE 480 AA; 55735 MW; 5DCAAE713436D04 CRC64;

Query Match 98.3%; Score 2507; DB 1; Length 480;
Best Local Similarity 98.1%; Pred. No. 7.3e-150;
Matches 471; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MSDVAIVKEGWLHKGGEYIKTRPRYFLKNDGTFIGYKERPDVDQREAPLNFSVAQC 60
Db 1 MNDVAIVKEGWLHKGGEYIKTRPRYFLKNDGTFIGYKERPDVDQREAPLNFSVAQC 60
```

QY 61 QLMKTERPRNTFIIRCLQWTTVIERTFHVETPEREETWTAIQTVDGLKKQBEEMDF 120  
 DB 61 QLMKTERPRNTFIIRCLQWTTVIERTFHVETPEREETWTAIQTVDGLKKQBEEMDF 120  
 QY 121 RSGSPDSNGSABEEMVSLAKPKHRTVMNEFEYLKLLGKGTGKVLVKEKATGRYYAMKI 180  
 DB 121 RSGSPDSNGSABEEMVSLAKPKHRTVMNEFEYLKLLGKGTGKVLVKEKATGRYYAMKI 180  
 QY 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLS 240  
 DB 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLS 240  
 QY 241 RERFSEDRARFYGAEIVSALDYLHSEKNVYRDLLKLENLMDKDGHIKITDGLCKEGI 300  
 DB 241 RERFSEDRARFYGAEIVSALDYLHSEKNVYRDLLKLENLMDKDGHIKITDGLCKEGI 300  
 QY 301 KDGAATMTKTCGTPYLAPEVLEDNDYGRAVDWGLGVVYEMWCGRLPFYQNDHEKLPFL 360  
 DB 301 KDGAATMTKTCGTPYLAPEVLEDNDYGRAVDWGLGVVYEMWCGRLPFYQNDHEKLPFL 360  
 QY 361 ILMEIRFPRTLPPEAKSLGSLKPKQRLGGGSDAKETIMQHRFFAGIVWQHVYKK 420  
 DB 361 ILMEIRFPRTLPPEAKSLGSLKPKQRLGGGSDAKETIMQHRFFAGIVWQHVYKK 420  
 QY 421 LSPPEKPOVTSETDTRYDEEFTAQMITITPPDQDSMECVDSERPHPPQFSYASGTA 480  
 DB 421 LSPPEKPOVTSETDTRYDEEFTAQMITITPPDQDSMECVDSERPHPPQFSYASGTA 480

## RESULT 5

KRAC\_MOUSE STANDARD; PRT; 480 AA.  
 AC P31750; Q62274;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE RAC-alpha serine/threonine-protein kinase (EC 2.7.1.37) (RAC-PK-alpha)  
 DE (AKT1 kinase) (protein kinase B) (PKB) (C-AKT) (Thymoma viral proto-oncogene).  
 GN Name=Akt1; Synonyms=Akt, Rac;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_taxid=10090;  
 RN [1]  
 RP Bousquets X., Powell C.;  
 RA Submitted (JUN-1992) to the EMBL/GenBank/DBJ databases.  
 RL [2]  
 RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.  
 RC STRAIN=AKR/J; TISSUE=Thymus;  
 RX MEDLINE=93173519; PubMed=8437858;  
 RA Bellacosa A., Franke T.F., Gonzalez-Portal M.E., Datta K., Taguchi T.,  
 RA Gardner J., Cheng J.Q., Testa J.R., Teichlis P.N.;  
 RT "Structure, expression and chromosomal mapping of c-akt: relationship  
 RT to v-akt and its implications.";  
 RL Oncogene 8:745-754(1993).  
 CC -!- FUNCTION: General protein kinase capable of phosphorylating  
 CC several known proteins.  
 CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear after activation by  
 CC integrin-linked protein kinase 1 (ILK1) (By similarity).  
 CC -!- TISSUE SPECIFICITY: Widely expressed. Low levels found in liver  
 CC with slightly higher levels present in thymus and testis.  
 CC -!- DOMAIN: Binding of the PH domain to the phosphatidylinositol 3-  
 CC kinase alpha (PI(3)K) results in its targeting to the plasma  
 CC membrane.  
 CC -!- PTM: Phosphorylation on Thr-308, Ser-473 and Tyr-474 is required  
 CC for full activity.  
 CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. RAC  
 CC subfamily.  
 CC -!- SIMILARITY: Contains 1 PH domain.

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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; M94335; AAA18254.1; -;  
 DR EMBL; X65687; CAA46620.1; -;  
 DR PIR; S33364; S33364.  
 DR HSSP; P31749; 1H10.  
 DR MGD; MGI:87986; Akt1.  
 DR GO; GO:0005737; C:cytoplasm; IDA.  
 DR GO; GO:0005515; F:protein binding; IPI.  
 DR GO; GO:0006915; P:apoptosis; IDA.  
 DR GO; GO:0008637; P:apoptotic mitochondrial changes; IDA.  
 DR GO; GO:0007281; P:germ-cell development; IDA.  
 DR GO; GO:0006488; P:protein amino acid phosphorylation; IDA.  
 DR GO; GO:0030163; P:protein catabolism; IDA.  
 DR GO; GO:0016567; P:protein ubiquitination; IDA.  
 DR InterPro; IPR011009; Kinase\_like.  
 DR InterPro; IPR001849; PH.  
 DR InterPro; IPR011036; PH related.  
 DR InterPro; IPR000961; PKinase C.  
 DR InterPro; IPR000719; Prot\_Kinase.  
 DR InterPro; IPR008271; Ser\_thr\_pkin AS.  
 DR InterPro; IPR002290; Ser\_thr\_pkinase.  
 DR Pfam; PF00169; PH; 1.  
 DR Pfam; PF00069; Pkinase; 1.  
 DR Pfam; PF00433; Pkinase\_C; 1.  
 DR ProDom; PD000001; Prot\_Kinase; 1.  
 DR SMART; SM00233; PH; 1.  
 DR SMART; SM00133; S\_TK\_X; 1.  
 DR SMART; SM00220; S\_TK; 1.  
 DR PROSITE; PS50003; PH DOMAIN; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS00101; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 DR ATP-binding; Phosphorylation; Serine/threonine-protein kinase;  
 KW Transferase.  
 FT DOMAIN 5 108 PH  
 FT DOMAIN 150 408 Protein kinase.  
 FT NP\_BIND 156 164 ATP (By similarity).  
 FT BINDING 179 179 ATP (By similarity).  
 FT ACT\_SITE 274 274 Proton acceptor (By similarity).  
 FT MOD\_RES 308 308 Phosphothreonine (by PDPK1) (By  
 FT similarity).  
 FT MOD\_RES 473 473 Phosphoserine (by ILK1) (By similarity).  
 FT MOD\_RES 474 474 Phosphotyrosine (By similarity).  
 FT CONFLICT 367 367 A -> R (in Ref. 2).  
 SQ SEQUENCE 480 AA; 55622 MW; 18D21018593B5A98 CRC64;  
 Query Match 98.2%; Score 2503; DB 1; Length 480;  
 Best Local Similarity 98.1%; Pred. No. 1.3e-149;  
 Matches 471; Conservative 3; Mismatches 6; Indels 0; Gaps 0;  
 QY 1 MSDVAIVKEGWLHKRGYIKTWPRYFLKNDGTFIGYKERPDVDQREAPLNFSVAQC 60  
 DB 1 MNDVAIVKEGWLHKRGYIKTWPRYFLKNDGTFIGYKERPDVDQREAPLNFSVAQC 60  
 QY 61 QLMKTERPRNTFIIRCLQWTTVIERTFHVETPEREETWTAIQTVDGLKKQBEEMDF 120  
 DB 61 QLMKTERPRNTFIIRCLQWTTVIERTFHVETPEREETWTAIQTVDGLKKQBEEMDF 120  
 QY 121 RSGSPDSNGSABEEMVSLAKPKHRTVMNEFEYLKLLGKGTGKVLVKEKATGRYYAMKI 180  
 DB 121 RSGSPDSNGSABEEMVSLAKPKHRTVMNEFEYLKLLGKGTGKVLVKEKATGRYYAMKI 180  
 QY 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLS 240  
 DB 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLS 240

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Qy 241 RRVFSDRFRFYGAIEVSALDYHSEKNVYVRDLKLENMLDKDGHKIKITDFGLCKEGI 300
Db 241 RRVFSDRFRFYGAIEVSALDYHSEKNVYVRDLKLENMLDKDGHKIKITDFGLCKEGI 300

Qy 301 KDGATMKTFCGTPPYLAPEVLENDYGRAVDWGLGVVYEMMCGRLPFYVQDHEKLFEL 360
Db 301 KDGATMKTFCGTPPYLAPEVLENDYGRAVDWGLGVVYEMMCGRLPFYVQDHEKLFEL 360

Qy 361 ILMEIEIRPPRTLGPBKAISLLSGLLKDDPKORLGGGSEDAKEIMQHRFFAGIIVQHVYVYKK 420
Db 361 ILMEIEIRPPRTLGPBKAISLLSGLLKDDPKORLGGGSEDAKEIMQHRFFAGIIVQHVYVYKK 420

Qy 421 LSPFPKQVTSSETDTRYFDEEFTAQMITITPPDQDDSMCEVDSERRRPHFPQFSYSASGTA 480
Db 421 LSPFPKQVTSSETDTRYFDEEFTAQMITITPPDQDDSMCEVDSERRRPHFPQFSYSASGTA 480

RESULT 6
O57513 PRELIMINARY; PRT; 480 AA.
AC O57513
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Serine/threonine protein kinase.
GN Name=akt1;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Theelen M., Swinkels S.U.M., de Jong M.D.M., Thomas A.A.M.,
RA Verkley A.J., Hanafusa H., Hummel B.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
CC -I- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC -I- SIMILARITY: Contains 1 PH domain.
DR EMBL; AF039943; AAB94767.1; -.
DR HSSP; P31749; IHI0.
DR GO; GO:000524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase_like.
DR InterPro; IPR001849; PH.
DR InterPro; IPR011036; PH related.
DR InterPro; IPR000961; Pkinase C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_Thr_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF00169; PH; 1.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF00433; Pkinase C; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SMO0233; PH; 1.
DR SMART; SMO0220; S_TKc; 1.
DR SMART; SMO0133; S_TK X; 1.
DR PROSITE; PS00003; PH DOMAIN; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 480 AA; 55723 MW; 3883A47FD6689626 CRC64;

Query Match 96.6%; Score 2464; DB 2; Length 480;
Best Local Similarity 96.0%; Pred. No. 3.7e-147;
Matches 461; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

Qy 1 MSDAIVKEGWLHKGVEIKTWRRPYRFLKNDGTFIGYKERPDQVDQREAPLNFSVAQC 60
Db 1 MNEVAIVKEGWLHKGVEIKTWRRPYRFLKNDGTFIGYKERPDQVDQREAPLNFSVAQC 60

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Qy 61 QLMKTERPRENTFIIRCLQMTTIVERTFHVETPEEREEMTTAQTQVADGLKKQEEEMDF 120
Db 61 QLMKTERPKENTFIIRCLQMTTIVERTFHVETPEEREEMTTAQTQVADSLKKQEEEMDF 120

Qy 121 RSGSPSDNSGAEMEVSIAKPKHRVTMNEFEYILKLKGKTFGKVILYKVKATGRYYAMKI 180
Db 121 RSGSPSDNSGAEMEVSMTKPKHVTMNEFEYILKLKGKTFGKVILYKVKATGRYYAMKI 180

Qy 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGSLFPHLS 240
Db 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGSLFPHLS 240

Qy 241 RRVFSDRFRFYGAIEVSALDYHSEKNVYVRDLKLENMLDKDGHKIKITDFGLCKEGI 300
Db 241 RRVFSDRFRFYGAIEVSALDYHSEKNVYVRDLKLENMLDKDGHKIKITDFGLCKEGI 300

Qy 301 KDGATMKTFCGTPPYLAPEVLENDYGRAVDWGLGVVYEMMCGRLPFYVQDHEKLFEL 360
Db 301 KDGATMKTFCGTPPYLAPEVLENDYGRAVDWGLGVVYEMMCGRLPFYVQDHEKLFEL 360

Qy 361 ILMEIEIRPPRTLGPBKAISLLSGLLKDDPKORLGGGSEDAKEIMQHRFFAGIIVQHVYVYKK 420
Db 361 ILMEIEIRPPRTLGPBKAISLLSGLLKDDPKORLGGGSEDAKEIMQHRFFAGIIVQHVYVYKK 420

Qy 421 LSPFPKQVTSSETDTRYFDEEFTAQMITITPPDQDDSMCEVDSERRRPHFPQFSYSASGTA 480
Db 421 LVPFPKQVTSSETDTRYFDEEFTAQMITITPPDQDDSMCEVDSERRRPHFPQFSYSASGTA 480

RESULT 7
KRAC_BOVIN
ID KRAC_BOVIN STANDARD; PRT; 480 AA.
AC Q01314;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE RAC-alpha serine/threonine-protein kinase (EC 2.7.1.37) (RAC-PK-alpha)
DE (Protein kinase B) (PKB).
GN Name=AKT1; Synonyms=PKB;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92037600; PubMed=1718748;
RA Coffey P.J., Woodgett J.R.;
RT "Molecular cloning and characterisation of a novel putative protein-
RT serine kinase related to the CAMP-dependent and protein kinase C
RT families."
RL Eur. J. Biochem. 201:475-481(1991).
RN [2]
RP REVISIONS.
RX MEDLINE=9249329; PubMed=1533586;
RA Coffey P.J., Woodgett J.R.;
RL Eur. J. Biochem. 205:1217-1218(1992).
CC -I- FUNCTION: General protein kinase capable of phosphorylating
CC several known proteins.
CC -I- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -I- SUBCELLULAR LOCATION: Cytoplasmic and nuclear after activation by
CC integrin-linked protein kinase 1 (ILK).
CC -I- DOMAIN: Binding of the PH domain to the phosphatidylinositol 3-
CC kinase alpha (PI(3)K) results in its targeting to the plasma
CC membrane.
CC -I- PTM: Phosphorylation on Thr-308, Ser-473 and Tyr-474 is required
CC for full activity.
CC -I- SIMILARITY: Belongs to the Ser/Thr protein kinase family. RAC
CC subfamily.
CC -I- SIMILARITY: Contains 1 PH domain.

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DR EMBL; X61036; CAN43371.1; -.
DR PIR; S62117; S62117.
DR HSSP; P31749; 1H10.
DR InAct; Q01314; -.
DR InterPro; IPR011009; Kinase_like.
DR InterPro; IPR001849; PH_related.
DR InterPro; IPR011036; PH_related.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00169; PH; 1.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF00433; Pkinase_C; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00233; PH; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS50003; PH_DOMAIN; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Phosphorylation; Serine/threonine-protein kinase;
KW Transferase.
FT DOMAIN 5 108 PH.
FT NP_BIND 150 408 Protein kinase.
FT BINDING 156 164 ATP (By similarity).
FT ACT_SITE 274 274 ATP (By similarity).
FT ACT_SITE 274 274 Proton acceptor (By similarity).
FT MOD_RES 308 308 Phosphothreonine (by PDK1).
FT MOD_RES 473 473 Phosphoserine (by ILK1).
FT MOD_RES 474 474 Phosphotyrosine (by similarity).
SQ SEQUENCE 480 AA; 55617 MW; 0BACA4123ED5A848 CRC64;
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Query Match 96.2%; Score 2452; DB 1; Length 480;
Best Local Similarity 96.2%; Pred. No. 2.1e-146;
Matches 462; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

Qy 1 MSDVAIVKEGWLKRGGEYIKTRPRYFLKNDGTFIGYKERPDQVDQREAPLNFSVAQC 60
Db 1 MNDVAIVKEGWLKRGGEYIKTRPRYFLKNDGTFIGYKERPDQLEQREAPLNFSVAQC 60

Qy 61 QLMKTERPRNTFIIRCLQWTVIERTPHVETPEREETWTAIQTVADGLKQEEEMDF 120
Db 61 QLMKTERPRNTFIIRCLQWTVIERTPHVETPEREETWTAIQTVADGLKQEEEMDF 120

Qy 121 RSGSPDNGSGAEEMVSLAKPKHRTVMNEFEYLLKLGKGTGKVLVKEKATGYAMK 180
Db 121 RSGSPGNSGAEEMVSLAKPKHRTVMNEFEYVLLKLGKGTGKVLVKEKATAAYAMK 180

Qy 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALYKYSFQTHDRLCFVMEYANGGELFFHLS 240
Db 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPSLTALYKYSFQTHDRLCFVMEYANGGELFFHLS 240

Qy 241 RERVFSDDRARFYGAEIVSALDYHSEKQVYVRDLKLENLMDKDGHIKITDFGLCKEGI 300
Db 241 RERVFSDDRARFYGAEIVSALDYHSEKEVYVRDLKLENLMDKDGHIKITDFGLCKEGI 300

Qy 301 KDGATMTKTCCTPEYLAPEVLNDYGRADVWGLGVVYEMWCGRLPFYVQDHEKLFEL 360
Db 301 KDGATMTKTCCTPEYLAPEVLNDYGRADVWGLGVVYEMWCGRLPFYVQDHEKLFEL 360

Qy 361 ILMBEIRPRTLPGPEAKSLLSGLLKDPKQRLGGSEDAKSIQHRFPFAGVWQHVYEKK 420
Db 361 ILMBEIRPRTLPGPEAKSLLSGLLKDPKQRLGGSEDAKSIQHRFPFASIVQDVYEKK 420
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Qy 421 LSPPPKQVTSSETDTRFYDEFTTAQMITITPPDQDSDMECVDSRRRPHFPQFSASCTA 480
Db 421 LSPPPKQVTSSETDTRFYDEFTTAQMITITPPDQDSDMEGVDSRRRPHFPQFSASATA 480

RESULT 8
Q98TY9 PRELIMINARY; PRT; 481 AA.
AC Q98TY9,
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Akt.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Andersen C.B., Sakae H., Roth R.A., Conti M.;
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC -!- SIMILARITY: Contains 1 PH domain.
DR EMBL; AF317656; AAC59601.1; -.
DR HSSP; P31751; IMRY.
DR GO; GO:000524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:000468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase_like.
DR InterPro; IPR001849; PH.
DR InterPro; IPR011036; PH_related.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF00169; PH; 1.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF00433; Pkinase_C; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00233; PH; 1.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00133; S_TK_X; 1.
DR PROSITE; PS50003; PH_DOMAIN; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 481 AA; 56042 MW; FF56CFB9A6454303 CRC64;
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Query Match 93.3%; Score 2378.5; DB 2; Length 481;
Best Local Similarity 93.1%; Pred. No. 9e-142;
Matches 448; Conservative 15; Mismatches 17; Indels 1; Gaps 1;

Qy 1 MSDVAIVKEGWLKRGGEYIKTRPRYFLKNDGTFIGYKERPDQVDQREAPLNFSVAQC 60
Db 1 MNEVAIVKEGWLKRGGEYIKTRPRYFLKSDGTFIGYKERPDQDQLETPLNFSVAKC 60

Qy 61 QLMKTERPRNTFIIRCLQWTVIERTPHVETPEREETWTAIQTVADGLKQEEEMDF 120
Db 61 QLMKTERPKNTFIIRCLQWTVIERTPHVDSPEEREEMIQVIQHVADNLKQEEEMNEV 120

Qy 121 RSG-SPDNGSGAEEMVSLAKPKHRTVMNEFEYLLKLGKGTGKVLVKEKATGYAMK 179
Db 121 RSGDSPDNGSGAEEMVSHSKPKHRTVMNEFEYLLKLGKGTGKVLVKEKATGYAMK 180

Qy 180 ILKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALYKYSFQTHDRLCFVMEYANGGELFFHL 239
Db 181 ILKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALYKYSFQTHDRLCFVMEYANGGELFFHL 240

Qy 240 SRRVFSDDRARFYGAEIVSALDYHSEKQVYVRDLKLENLMDKDGHIKITDFGLCKEG 299
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Db 241 SRERIFSEDRARFYCAETVSALDYLHSEKNVYVRDLKLENLMLDKGHKITDPLGCKEG 300
Qy 300 IKDGTATWKTTCGTPYLAPEVLNDYGRADVWGLGVVYEMWCGRLPFVNDQHEKLF 359
Db 301 IKDGTATWKTTCGTPYLAPEVLNDYGRADVWGLGVVYEMWCGRLPFVNDQHEKLF 360
Qy 360 LILMEEIRFRTLTGLPEAKSLSLGLKKDPKQRLGGSGSEDAKEIMQHRFFAGIVMQRHYVEK 419
Db 361 LILMEEIRFRTLTGLPEAKSLSLGLKKDPKQRLGGSPDDAKEINQHKFFAGIVWQYVEK 420
Qy 420 KLSPPFPQVTSQTDTRYFDBEFTAQMTITPPQDDSMCEVCDSERPHPPQFSYSASGT 479
Db 421 KLVPFPQVTSQTDTRYFDBEFTAQMTITPPQDDNFVNDNERRPHPPQFSYSASGN 480
Qy 480 A 480
Db 481 A 481

RESULT 9
Q8BS26 PRELIMINARY; PRT; 452 AA.
AC Q8BS26;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus adult male aorta and vein cDNA, RIKEN full-length
DE enriched library, clone:A330023F15 product:thymoma viral proto-
DE oncogene 1, full insert sequence.
GN Name=Akt1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP STRAIN=C57BL/6J; TISSUE=Aorta and vein;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayaashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Mech. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Aorta and vein;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN PANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Aorta and vein;
RA The FANTOM Consortium;
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RL 60,770 full-length cDNAs.";
RN [4]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Aorta and vein;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayaashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Aorta and vein;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Saeki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuami T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

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RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Tanaka M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayaashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RL sequencing pipeline with 384 multicapillary sequencer.";
RN Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Aorta and vein;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayaashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Saeki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayaashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC -1- SIMILARITY: Contains 1 PH domain.
DR EMBL; AK040758; BAC30695.1; -.
DR HSSP; P31749; 1H10.
DR MGD; MGI:87986; Akt1.
DR GO; GO:0005737; Cytoplasm; IDA.
DR GO; GO:0030027; Cilamellipodium; IDA.
DR GO; GO:0005515; F-protein binding; IPI.
DR GO; GO:0004672; F-protein kinase activity; IDA.
DR GO; GO:0006915; P-apoptosis; IDA.
DR GO; GO:0008637; P-apoptotic mitochondrial changes; IDA.
DR GO; GO:0007281; P-germ cell development; IDA.
DR GO; GO:0043066; P-negative regulation of apoptosis; IDA.
DR GO; GO:0006468; P-protein amino acid phosphorylation; IDA.
DR GO; GO:0030163; P-protein catabolism; IDA.
DR GO; GO:0016567; P-protein ubiquitination; IDA.
DR InterPro; IPR011009; Kinase_like.
DR InterPro; IPR001849; PH.
DR InterPro; IPR011036; PH-related.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_Thr_kinase.
DR Pfam; PF00169; PH; 1.
DR Pfam; PF00089; Pkinase; 1.
DR Pfam; PF00433; Pkinase_C; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00233; PH; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00133; S_TKc; 1.
DR PROSITE; PS00003; PH_DOMAIN; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 452 AA; 52618 MW; E203C8F46A18E55E CRC64;

Query Match 90.3%; Score 2303; DB 2; Length 452;
Best Local Similarity 98.0%; Pred. No. 4.8e-137;
Matches 433; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MSDVAIVKEGWLHKGREYIKTWPRVFLKNDGCTFGYKERPDVDQREAPLNFSVAQC 60
Db 1 MNDVAIVKEGWLHKGREYIKTWPRVFLKNDGCTFGYKERPDVDQREAPLNFSVAQC 60
Qy 61 QLMKTERPRNTFIIRCLQWTTVIERTFHVETPEEREETWTAIQTVDAGLKKOESEEMDF 120
Db 61 QLMKTERPRNTFIIRCLQWTTVIERTFHVETPEEREETWTAIQTVDAGLKKOESEEMDF 120
Qy 121 RSGSPDNGSAGEMEVSLAKPKHRVTWNEPEYIKLJGKTFGKVLVKEKATGRYYAMKI 180

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Db 121 RSGSPSDNSGAEEMVSLAKPKHRTVMNEPEYLVKLGKGTGKVLVKEKATGRYAMKI 180  
 Qy 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGBELFPHLS 240  
 Db 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGBELFPHLS 240  
 Qy 241 RERFSEDRARFYGAIEVSALDYHSEKQNVYRDLKLENLMDKDGHIKITDFGLCKEGI 300  
 Db 241 RERFSEDRARFYGAIEVSALDYHSEKQNVYRDLKLENLMDKDGHIKITDFGLCKEGI 300  
 Qy 301 KGDATMTKTCGTPPEYLAPEVLENDNDYGRAVDWGLGVVYEMVCGRLPFYVQDHEKLP 360  
 Db 301 KGDATMTKTCGTPPEYLAPEVLENDNDYGRAVDWGLGVVYEMVCGRLPFYVQDHEKLP 360  
 Qy 361 ILMEIRPPRTLGPEAKSLLSGLLKDPKQBLGGGSEDAKIMQHRFPAGIYVQHVYBK 420  
 Db 361 ILMEIRPPRTLGPEAKSLLSGLLKDPKQBLGGGSEDAKIMQHRFPAGIYVQHVYBK 420  
 Qy 421 LSPFPKPOVTSETDTRYDEEP 442  
 Db 421 LSPFPKPOVTSETDTRYDEEP 442

## RESULT 10

AKT2\_MOUSE  
 ID AKT2\_MOUSE STANDARD; PRT; 481 AA.  
 AC Q60823;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE RAC-beta serine/threonine-protein kinase (EC 2.7.1.37) (RAC-PK-beta)  
 DE (Protein kinase Akt-2) (Protein kinase B, beta) (PKB beta).  
 GN Name=Akt2;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6 X CBA; TISSUE=Thymus;  
 RX MEDLINE=96032568; PubMed=7566964;  
 RA Altomare D.A., Guo K., Cheng J.Q., Sonoda G., Waleh K., Testa J.R.;  
 RT "Cloning, chromosomal localization and expression analysis of the  
 mouse Akt2 oncogene";  
 RL Oncogene 11:1055-1060(1995).  
 RN [2]

RP SEQUENCE FROM N.A.  
 RC TISSUE=Retina, and Salivary gland;  
 RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.B., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,  
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo A.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly P.H.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Faney J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smallos D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -!- FUNCTION: General protein kinase capable of phosphorylating  
 several known proteins  
 CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphorylated  
 CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. RAC

CC subfamily.  
 CC -!- SIMILARITY: Contains 1 PH domain.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; U22445; AAA3557.1; --  
 CC EMBL; BC026151; AAH26151.1; --  
 CC EMBL; BC040377; AAH40377.1; --  
 CC HSPF; P31751; IGZK.  
 CC MGD; MGI:104874; Akt2.  
 CC InterPro; IPR011009; Kinase\_like.  
 CC InterPro; IPR001849; PH.  
 CC InterPro; IPR011036; PH related.  
 CC InterPro; IPR000961; Kinase\_C.  
 CC InterPro; IPR000719; Prot\_kinase.  
 CC InterPro; IPR008271; Ser\_thr\_kin\_AS.  
 CC Pfam; PF00169; PH; 1.  
 CC Pfam; PF00069; Pkinase; 1.  
 CC Pfam; PF00433; Pkinase\_C; 1.  
 CC ProDom; PD000001; Prot\_kinase; 1.  
 CC PROSITE; PS00003; PH DOMAIN; 1.  
 CC PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
 CC PROSITE; PS00113; PROTEIN KINASE DOM; 1.  
 CC PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 CC ATP-binding; Serine/threonine-protein kinase; Transferase.  
 KW DOMAIN 5 108 PH.  
 FT DOMAIN 152 409. Protein kinase.  
 FT NP\_BIND 158 166 ATP (By similarity).  
 FT BINDING 181 181 ATP (By similarity).  
 FT ACT\_SITE 275 275 Proton acceptor (By similarity).  
 SQ SEQUENCE 481 AA; 55741 MW; 4849A9C4FB9CFA7D CRC64;

Query Match 83.5%; Score 2128.5; DB 1; Length 481;  
 Best Local Similarity 81.8%; Pred. No. 5e-126;  
 Matches 392; Conservative 52; Mismatches 32; Indels 3; Gaps 2;  
 Qy 1 MSDVAIVKEGWLHKGGEYIKTRPRYFLKNDGTGFGYKERPDQVDQREAPLNPFVAC 60  
 Db 1 MNEVSVIKEGWLHKGGEYIKTRPRYFLKSDGSGFYGERPEAPDQTLPLNPFVAC 60  
 Qy 61 QLMKTERPRNTFIRCLQWTTVIERTPHVTPEBEREWTTAQTADGLKKQ--EEEM 118  
 Db 61 QLMKTERPRNTFVIRCLQWTTVIERTFHVDSPDEREEMWAIQVANSLKQRGEDAM 120  
 Qy 119 DFRSGSPSDNSGAEEMVSLAKPKHRTVMNEPEYLVKLGKGTGKVLVKEKATGRYAM 178  
 Db 121 DYKCGSPSDSSTSEMEVAVNKAARAKVTMNDFDYLLKLGKGTGKVLVKEKATGRYAM 180  
 Qy 179 KILKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGBELFPH 238  
 Db 181 KILKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYAFQTHDRLCFVMEYANGBELFPH 240  
 Qy 239 LSRERFSEDRARFYGAIEVSALDYHSEKQNVYRDLKLENLMDKDGHIKITDFGLCKE 298  
 Db 241 LSRERFSEDRARFYGAIEVSALDYHSEKQNVYRDLKLENLMDKDGHIKITDFGLCKE 299  
 Qy 299 GIKDGMATKTCGTPPEYLAPEVLENDNDYGRAVDWGLGVVYEMVCGRLPFYVQDHEKLP 358  
 Db 300 GISDGMATKTCGTPPEYLAPEVLENDNDYGRAVDWGLGVVYEMVCGRLPFYVQDHEKLP 359  
 Qy 359 ELIIMEIRPPRTLGPEAKSLLSGLLKDPKQBLGGGSEDAKIMQHRFPAGIYVQHVYBK 418  
 Db 360 ELIIMEIRPPRTLGPEAKSLLSGLLKDPKQBLGGGSEDAKIMQHRFPAGIYVQHVYBK 419  
 Qy 419 KKLSPFPKPOVTSETDTRYDEEPTAQMITTPPDQDSDMECVDSERPHPPQPSYSAS 477  
 Db 420 KKLSPFPKPOVTSETDTRYDEEPTAQMITTPPDQDSDMECVDSERPHPPQPSYSAS 478

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RESULT 11
ID AKT2_HUMAN STANDARD; PRT; 481 AA.
AC P31751.
DT 01-JUN-1993 (Rel. 26, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE RAC-beta serine/threonine-protein kinase (SC 2.7.1.37) (RAC-PK-beta)
DE (Protein kinase Akt-2) (Protein kinase B, beta) (PKB beta).
GN Name-AKT2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Epithelium;
RX MEDLINE=9219987; PubMed=1801921;
RA Jones P.F., Jakubowicz T., Hemmings B.A.;
RT "Molecular cloning of a second form of rac protein kinase.";
RL Cell Regul. 2:1001-1009(1991).
RV [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93028445; PubMed=1409633;
RA Cheng J.Q., Godwin A.K., Bellacosa A., Taguchi T., Franke T.F.,
RA Hamilton T.C., Taichlis P.N., Testa J.R.;
RT "AKT2, a putative oncogene encoding a member of a subfamily of
RT protein-serine/threonine kinases, is amplified in human ovarian
RT carcinomas.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:9267-9271(1992).
CC -1- FUNCTION: General protein kinase capable of phosphorylating
CC several known proteins.
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- TISSUE SPECIFICITY: In all human cell types so far analyzed.
CC -1- DISEASE: Alterations of AKT2 may contribute to the pathogenesis of
CC ovarian carcinomas.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. RAC
CC subfamily.
CC -1- SIMILARITY: Contains 1 PH domain.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M71198; AAA36585.1; -.
CC EMBL; M95936; AAA58364.1; -.
CC PIR; A46288; A46288.
CC PDB; 1GZK; X-ray; A=146-459.
CC PDB; 1GZN; X-ray; A=146-480.
CC PDB; 1GZO; X-ray; A=146-459.
CC PDB; 1MRV; X-ray; A=143-481.
CC PDB; 1MRV; X-ray; A=143-481.
CC InAct; P31751; -.
CC Genes; HGNC:392; AKT2.
CC MIM; 164731; -.
CC GO; GO:0004674; F:protein serine/threonine kinase activity; TAS.
CC GO; GO:0006464; P:protein modification; TAS.
CC InterPro; IPR011009; Kinase_like.
CC InterPro; IPR001849; PH.
CC InterPro; IPR011036; PH_related.
CC InterPro; IPR000961; Pkinase_C.
CC InterPro; IPR000719; Prot_kinase.
CC InterPro; IPR008271; Ser_thr_pkin_AS.
CC InterPro; IPR002290; Ser_thr_kinase.
CC Pfam; PF00169; PH; 1.
CC Pfam; PF00069; Pkinase; 1.
CC Pfam; PF00433; Pkinase_C; 1.
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DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SMO0233; PH; 1.
DR SMART; SMO0133; S_TK_X; 1.
DR SMART; SMO0220; S_TKG; 1.
DR PROSITE; PS50003; PH DOMAIN; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW 3D-structure; ATP-binding; Serine/threonine-protein kinase;
KW Transferase.
FT DOMAIN 5 108 PH.
FT DOMAIN 152 409 Protein kinase.
FT NP_BIND 158 166 ATP (By similarity).
FT BINDING 181 181 ATP (By similarity).
FT ACT_SITE 275 275 Proton acceptor (By similarity).
FT CONFLICT 478 481 SIRE -> FREEVDLLMSLVSLPDLPSDFSLKSHSPSSNF
FT ILLSFSLKK (in Ref. 1)
SQ SEQUENCE 481 AA; 55768 MW; B18C87A7246FB24 CRC64;
Query Match 83.4%; Score 2126.5; DB 1; Length 481;
Best Local Similarity 81.6%; Pred. No. 6.7e-126;
Matches 391; Conservative 52; Mismatches 33; Indels 3; Gaps 2;
Qy 1 MSDVAIVKGLHKGGEYIKTWPRPYLLKNDGTFYKRPDPVDQREAPLNFSVAQC 60
Db 1 MNEVSIKEGWLHKGGEYIKTWPRPYLLKSDGSFYKRPDPQDTLPNNFSVAEC 60
Qy 61 QLMKTERPRNTFIIRCLQWTVIERTFHVETPEEREETTAIQTVADGLKKOE--EEM 118
Db 61 QLMKTERPRNTFIIRCLQWTVIERTFHVDSFDREEMWRAIQMVANSUKQAPGEDPM 120
Qy 119 DFRSGSPSDNSGAEMEVSLLAKPKRVTMNEFEYLKLLGKGTGKVLVKEKATGRYYAM 178
Db 121 DYKCGSPSDSSTTEMEVAVSKAKVYMWDFYLLKLGKGTGKVLVKEKATGRYYAM 180
Qy 179 KILKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSPOTDRLCFVMEYANGGELFFH 238
Db 181 KILKKEVIVAKDEVAHTVTSRVLQNRHPFLTALKYAFQTHDLRCFVMEYANGGELFFH 240
Qy 239 LSRERFVEDRARPFGAEIVSALDYHSEKNVYVRLKLENMLDKDGHKIKITDFGLCKE 298
Db 241 LSRERFVEERARPFGAEIVSALEYLHS-RDYYRDLKLENMLDKDGHKIKITDFGLCKE 299
Qy 299 GIKDGATMTKTCGTPEYLAPEVLEDNDYGRAVDWGLGVVYEMVCMGRLPFYQDHEKLF 358
Db 300 GISDGTMTKTCGTPEYLAPEVLEDNDYGRAVDWGLGVVYEMVCMGRLPFYQDHERLF 359
Qy 359 ELILMBEIRPRTILGPEAKSLLSGLLKQDPKQRLGGSEDAKIMQHRFPAGIVQHYVE 418
Db 360 ELILMBEIRPRTILSPEAKSLLAGLLKQDPKQRLGGSPDAKEVMEHRFFLSINWQDVQ 419
Qy 419 KKLSPKPKQVTSSTETRYFEDEBFTAQMITTPDDDDSMCEYDSERRPHFPQFSYAS 477
Db 420 KKLPPKPKQVTSSEVDTRYFDEBFTAQSIITPPDRYDSLGLLELDQRTTHFPQFSYAS 478
RESULT 12
Q7ZX15
ID Q7ZX15 PRELIMINARY; PRT; 486 AA.
AC Q7ZX15;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Akt2-prov protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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61 EQQJMKTERPRPNTFVIRCLQWTTVIERFHVDTPEERBEWIIAIIQTVANGLKNQVPEDE 120  
 114 EEEEMDFRSGSPSDNSGABEMEVSIAKPKHRVTMNEFEYLKLGKGTGFKVILVKEKATG 173  
 121 EEEAMEVKYGPSDSVSSAEQMDVAMSKGHPKVTMNDFDYLLKLGKGTGFKVILVREKATG 180  
 174 RYYAMKILKEVIVAKDEVAHTLTENRVLONSHPHFLTALKYSFOTHDRILCFVMEYANGG 233  
 181 RYYAMKILKEVIAKDEVAHTLTESRVLTQNTKHPFLTALKYAFQTSDDRLCFVMEYANGG 240  
 234 ELUPFHLSRERVTFSEDRARFYGAIVSALDYLSHSEKNVVRDLKLENLMLDKDGHKIKITDF 293  
 241 ELUPFHLSRERVTFEDRARRFYGAIVSALDYLSHLS-RNVVYRDIKLENLMLDKDGHVKITDF 299  
 294 GLCKEGIKDGATMKTCGTPYLAPEVLENDNYGRAVDMWMLGVLVVMYEMMCGRLPFYNQD 353  
 300 GLCKEGITDGATWRTTCGTPYLAPEVLENDNYGRAVDMWMLGVLVVMYEMMCGRLPFYNQD 359  
 354 HEKLPFLILMEEIRFPRTLGPEAKSLLSGLLKKDKPQRLGGSGSEDAKEINQHRFFAGIVW 413  
 360 HERLPFLILMEEIRFPRTLSPEAKSLLAGLLKKDKPQRLGGSGPNDAAQEVMSHRFPFVSINW 419  
 414 QHVVEKLLPPPKPQVTSSTDTRYFDEEPTAQMIIITTPDQDDSMECVDSERRPHFPQFS 473  
 420 QDVTERKLLPFPKPVQVTSIDTRYFDEEPTAQISITITPPDRYDNLDALESQDRPHFPQFS 479  
 474 YSAS 477  
 480 YSAS 483  
 RESULT 13  
 AKT2\_RAT  
 ID AKT2\_RAT STANDARD; PRT; 481 AA.  
 AC P47157;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE RAC-beta serine/threonine-protein kinase (EC 2.7.1.37) (RAC-PK-beta)  
 DE (Protein kinase Akt-2) (Protein kinase B, beta) (PKB beta).  
 GN Name:Akt2;  
 GN Rattus norvegicus (Rat).  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 ON NCBI\_TaxID=10116;  
 RX [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Testis;  
 RX MEDLINE=95091823; PubMed=7999118;  
 RA Konishi H., Shinomura T., Kuroda S.I., Ono Y., Kikkawa U.;  
 RT "Molecular cloning of rat RAC protein kinase alpha and beta and their  
 RT association with protein kinase C zeta.";  
 RL Biochem Biophys. Res. Commun. 205:817-825(1994).  
 CC -1- FUNCTION: General protein kinase capable of phosphorylating  
 CC several known proteins.  
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. RAC  
 CC subfamily.  
 CC -1- SIMILARITY: Contains 1 PH domain.  
 CC  
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 CC or send an email to [license@sib-ch](mailto:license@sib-ch)).  
 CC  
 CC EMBL; D300041; BAA06280.1; -  
 CC DR PIR; JC2438; JC2438.  
 CC DR HSP; P31751; IGZK.  
 CC DR RGD; 2082; Akt2.  
 CC DR InterPro; IPR011009; Kinase like.

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DR InterPro; IPR001849; PH.
DR InterPro; IPR011036; PH related.
DR InterPro; IPR000961; PKinase C.
DR InterPro; IPR000719; Prot_Kinase.
DR InterPro; IPR008271; Ser_thr_kin_AS.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00169; PH; 1.
DR Pfam; PF00069; PKinase; 1.
DR Pfam; PF00433; PKinase C; 1.
DR ProDom; PD000001; Prot_Kinase; 1.
DR SMART; SM002133; PH; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TK; 1.
DR PROSITE; PS00003; PH DOMAIN; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding; Serine/threonine-protein kinase; Transferase.
FT DOMAIN 5 108 PH.
FT NP_BIND 152 409 Protein kinase.
FT BINDING 181 181 ATP (By similarity).
FT ACT_SITE 275 275 Proton acceptor (By similarity).
SQ SEQUENCE 481 AA; 55343 MW; 3C4BB65B2F376F85 CRC64;

Query Match      82.9%; Score 2113.5; DB 1; Length 481;
Best Local Similarity 81.4%; Pred. No. 4.4e-125;
Matches 390; Conservative 52; Mismatches 34; Indels 3; Gaps 2;

Qy 1 MSQVAIVKEGHLHKGVEYIKTRPRYFLLNKDGTFYIGYKRPQVDQREAPLNFSVAQC 60
Db 1 MNEVSIVKEGHLHKGVEYIKTRPRYFLLNKDGTFYIGYKRPQVDQREAPLNFSVAEC 60

Qy 61 QLMKTERPRNTEIIRCLQWTTVIERTFHVETPEREETWTAIQTVADGKKQ--EEEM 118
Db 61 QLMKTERPRNTEIIRCLQWTTVIERTFHVDSPEREETWTAIQTVADGKKQ--EEEM 120

Qy 119 DFRSGSPDSNGABEMEVSIAKPKHRYTMNEFEYIKLLGKGTFGKVLVKEKATGRYYAM 178
Db 121 DYKSGSPDSSTSEMVEVAVSKARAKVTMDNDFYLLKLGKGTFGKVLVREKATGRYYAM 180

Qy 179 KILKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSPQTHDLRCFVMEYANGGELFFH 238
Db 181 KILKEVIVAKDEVAHTVTSRVLQNRHPFLTALKYAFQTHDLRCFVMEYANGGDLFFH 240

Qy 239 LSRERFSEDRARFYGAIEIVSALDYLSHSEKNVVDLKLLENLMDKDGHIKITDFGLCKE 298
Db 241 LSRERFTEDRARFYGAIEIVSALDYLSHS--TDVVTVDIKLENLMDKDGHIKITDFGLCKE 299

Qy 299 GIKDGATMKTFCGTFPEYLAPEVLDDNDYGRAVDWGLGVVYEMMCGRLPFYNQDHEKLF 358
Db 300 GISDGATMKTFCGTFPEYLAPEVLDDNDYGRAVDWGLGVVYEMMCGRLPFYNQDHERLF 359

Qy 359 ELILMEIRPRTLGPEAKSLGGLKKPKQKRGSGGSDAKETMQHRFPAGIVQHVHYE 418
Db 360 ELILMEIRPRTLGPEAKSLGGLKKPKQKRGSGGSDAKETMQHRFPAGIVQHVHYE 419

Qy 419 KKLSPPEKQVTSFTDTRYFDEETFAQMITTPDDQDSDMECVDSERPPEPFSYSAS 477
Db 420 KKLSPPEKQVTSFTDTRYFDEETFAQMITTPDDRYDSLGSLDQRTHPQFSYSAS 478

RESULT 14
AKT3_HUMAN
AC Q91243; Q96QV3; Q9UFP5;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE RAC-gamma serine/threonine-protein kinase (EC 2.7.1.37) (RAC-PK-gamma)
DE (Protein kinase Akt-3) (Protein kinase B, gamma) (PKB gamma) (STK-2).
GN Name=AKT3;
OS Homo sapiens (Human).
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND MUTAGENESIS.
RX MEDLINE=99194749; PubMed=10092583; DOI=10.1074/jbc.274.14.9133;
RA Brodbeck D., Cron P., Hemmings B.A.;
RT "A human protein kinase B gamma with regulatory phosphorylation sites
RL in the activation loop and in the C-terminal hydrophobic domain.";
RN J. Biol. Chem. 274:9133-9136(1999).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99225329; PubMed=10208883; DOI=10.1006/bbrc.1999.0559;
RA Nakatani K., Sakaue H., Thompson D.A., Weigel R.J., Roth R.A.;
RT "Identification of a human Akt3 (protein kinase B gamma) which
RL contains the regulatory serine phosphorylation site.";
RN Biochem. Biophys. Res. Commun. 257:906-910(1999).
[3]
RP SEQUENCE FROM N.A.
RX TISSUE=Brain;
MEDLINE=99421751; PubMed=10491192;
RA Masure S., Haefner B., Wesselink J.-J., Hoefnagel E., Mortier E.,
Verhaesselt P., Tuytelaars A., Gordon R., Richardson A.;
RT "Molecular cloning, expression and characterization of the human
RL serine/threonine kinase Akt-3.";
RN Eur. J. Biochem. 265:353-360(1999).
[4]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Li X., Yu L., Huang H., Zhang M., Zhao Y., Zhao S.;
RT "Cloning of a novel human CDNA, STK-2, which encodes a rat serine-
RL threonine protein kinase (STK) homolog.";
RN Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
[5]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Testis;
RX MEDLINE=21154917; PubMed=11230166; DOI=10.1101/gr.154701;
RA Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S.,
Ansoerge W., Boecker M., Bloecker H., Bauersachs S., Blum H.,
Lauber J., Duesterhoef A., Beyer A., Koehrer K., Strack N.,
Mewes H.-W., Othenwaelder B., Obermaier B., Tampe J., Heubner D.,
Wambutt R., Korn B., Klein M., Foustka A.;
RT "Towards a catalog of human genes and proteins: sequencing and
RL analysis of 500 novel complete protein coding human cDNAs.";
RN Genome Res. 11:422-435(2001).
[6]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND MUTAGENESIS OF THR-305 AND
THR-447.
RX PubMed=11387345; DOI=10.1074/jbc.M104633200;
RA Brodbeck D., Hill M.M., Hemmings B.A.;
RT "Two splice variants of PKB gamma have different regulatory capacity
RL depending on the presence or absence of the regulatory phosphorylation
site Ser-472 in the C-terminal hydrophobic domain.";
RN J. Biol. Chem. 276:29550-29558(2001).
CC -1- FUNCTION: IGF-1 leads to the activation of AKT3, which may play a
CC role in regulating cell survival. Capable of phosphorylating
CC several known proteins. Truncated isoform 2/pKB gamma 1 without
CC the second serine phosphorylation site could still be stimulated
CC but to a lesser extent.
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic and membrane-associated after
CC cell stimulation leading to its translocation.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=PKB gamma;
CC IsoId=Q91243-1; Sequence=Displayed;
CC Name=2; Synonyms=PKB gamma 1;
CC IsoId=Q91243-2; Sequence=VSP_004947;
CC -1- TISSUE SPECIFICITY: In adult tissues, it is highly expressed in
CC brain, lung and kidney, but weakly in heart, testis and liver. In
CC fetal tissues, it is highly expressed in heart, liver and brain
CC and not at all in kidney.
CC -1- DOMAIN: Binding of the PH domain to the phosphatidylinositol 3-
CC kinase alpha (PI(3)K) results in its targeting to the plasma
```









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OM protein - protein search, using sw model

Run on: February 23, 2005, 20:38:14 : Search time 42 Seconds  
(without alignments)  
1099.620 Million cell updates/sec

Title: US-10-621-485A-1  
Perfect score: 2550  
Sequence: 1 MSDVAIVKEGWLKRGVEIK.....VDSRRPHFPQFSASGTA 480

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2544	99.8	480	1 A39360	protein kinase (EC
2	2509	98.4	480	1 S33364	protein kinase (EC
3	2509	98.4	763	1 A40831	gag-akt polyprotei
4	2507	98.3	480	1 J24337	protein kinase (EC
5	2452	96.2	480	1 S62117	protein kinase (EC
6	2126.5	83.4	481	1 A46288	protein kinase (EC
7	2113.5	82.9	481	1 J24338	protein kinase (EC
8	2105.5	82.6	479	1 A59380	protein kinase (EC
9	2008.5	78.8	462	1 T17287	protein kinase (EC
10	1989.5	78.0	454	1 J43435	protein kinase (EC
11	1581.5	62.0	611	1 A58888	protein kinase (EC
12	1490.5	58.5	546	1 T43233	protein kinase (EC
13	1470	57.6	541	1 T43232	protein kinase (EC
14	1390.5	54.5	528	1 T21523	protein kinase (EC
15	1324	51.9	483	1 T43234	protein kinase (EC
16	855	33.5	671	1 K1HUC1	protein kinase C (
17	854	33.5	736	1 K1RBC2	protein kinase C (
18	853	33.5	671	1 K1RBC1	protein kinase C (
19	853	33.5	1102	2 T28666	protein kinase C-r
20	852	33.4	431	2 A48094	serum and glucocor
21	852	33.4	671	1 K1RUC1	protein kinase C (
22	849.5	33.3	683	1 A23690	protein kinase (EC
23	848.5	33.3	737	1 K1M5CE	protein kinase C (
24	847.5	33.2	737	1 K1M5CE	protein kinase C (
25	845.5	33.2	682	1 S29478	protein kinase C (
26	842	33.0	682	1 A39666	protein kinase C (
27	840.5	33.0	737	1 K1RUC2	protein kinase C (
28	837	32.8	1096	1 S61917	protein kinase C (
29	833	32.7	1016	1 A46079	protein kinase C (

## RESULT 1

A39360  
protein kinase (EC 2.7.1.37) akt1 [validated] - human  
N;Alternate names: protein kinase B alpha; RAC-PK-alpha; serine/threonine-specific protease  
C;Species: Homo sapiens (man)  
C;Date: 20-Mar-1992 #sequence\_revision 12-May-1994 #text\_change 16-Aug-2004  
C;Accession: A39360; S36389; S18000; S20836  
R;Jones, P.F.; Jakubowicz, T.; Pitossi, F.J.; Maurer, F.; Hemmings, B.A.  
Proc. Natl. Acad. Sci. U.S.A. 88, 4171-4175, 1991  
A;Title: Molecular cloning and identification of a serine/threonine protein kinase of the  
A;Reference number: A39360; MUID:91239529; PMID:1851997  
A;Accession: A39360  
A;Molecule type: mRNA  
A;Residues: 1-480 <JON>  
A;Cross-references: UNIPROT:P31749; GB:M63167; NID:g190827; PIDN:AAA36539.1; PID:g190828  
R;Coffer, P.J.; Woodgett, J.R.  
Eur. J. Biochem. 205, 1217, 1992  
A;Reference number: S24423; MUID:92249329; PMID:1533586  
A;Contents: erratum  
A;Accession: S36389  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: mRNA  
A;Residues: 63-172, 'A', 175-201, 'Q', 203-211, 'R', 213-245, 'A', 247-408, 'T', 410-475, 'P', 477, '  
A;Cross-references: EMBL:X61037; NID:g35480; PIDN:CAA43372.1; PID:g35481  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1991  
R;Coffer, P.J.; Woodgett, J.R.  
Eur. J. Biochem. 201, 475-481, 1991  
A;Title: Molecular cloning and characterisation of a novel putative protein-serine kinase  
A;Reference number: S17999; MUID:92037600; PMID:1718748  
A;Accession: S18000  
A;Status: nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 63-70, 'TPSSAACSGPLSSNAPSMWRLRSGVDNRHDCGRRPQ', 'EAGGGDGLPVGLTQRLGRRDGGV'  
A;Cross-references: EMBL:X61037  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1991  
R;Coffer, P.  
submitted to the EMBL Data Library, July 1991  
A;Reference number: S20836  
A;Accession: S20836  
A;Molecule type: mRNA  
A;Residues: 63-70, 'TPSSAACSGPLSSNAPSMWRLRSGVDNRHDCGRRPQ', 'EAGGGDGLPVGLTQRLGRRDGGV'  
A;Cross-references: EMBL:X61037  
A;Note: this sequence has been revised in reference S24423  
R;Alessi, D.R.; Andjelkovic, M.; Caudwell, B.; Cron, P.; Morrice, N.; Cohen, P.; Hemmings  
EMBO J. 15, 6541-6551, 1996  
A;Title: Mechanism of activation of protein kinase B by insulin and IGF-1.  
A;Reference number: A64192; MUID:9713284; PMID:8978681  
A;Contents: annotation; phosphorylation sites  
R;Toker, A.; Newton, A.C.  
J. Biol. Chem. 275, 8271-8274, 2000

30	831.5	32.6	984	2	S67537	protein kinase (EC
31	828	32.5	547	2	T22856	hypothetical prote
32	828	32.5	988	1	S35382	protein kinase C (
33	826.5	32.4	586	2	A53758	protein kinase C (
34	826.5	32.4	587	2	A49509	protein kinase C (
35	826.5	32.4	634	1	B32392	protein kinase C (
36	826.5	32.4	673	1	K1HUC2	protein kinase C (
37	826.5	32.4	673	2	S11213	protein kinase C (
38	825	32.4	707	1	A53530	protein kinase C (
39	825	32.4	1174	2	T43051	protein kinase C (
40	824.5	32.3	673	1	K1RBC2	protein kinase C (
41	823.5	32.3	673	1	K1RUC2	protein kinase C (
42	823.5	32.3	673	1	K1BOC2	protein kinase C (
43	820.5	32.2	672	1	K1BOC	protein kinase C (
44	818.5	32.1	672	1	K1RUC	protein kinase C (
45	817.5	32.1	672	1	K1HUC4	protein kinase C (

## ALIGNMENTS

A;Title: Akt/protein kinase B is regulated by autophosphorylation at the hypothetical pS3364  
A;Reference numbers: A64193; MUID:20187529; PMID:10722653  
A;Contents: annotation; autophosphorylation site  
C;Comment: Akt1 is ubiquitous as an inactive multimeric complex. It binds phosphatidyl-3-nt protein kinase 1 complex. Akt1 can then autophosphorylate and become fully active.  
C;Genetics:  
A;Gene: GDB:AKT1; RAC; PKB  
A;Cross-references: GDB:118989; OMIM:164730  
A;Map position: 14q32.32-14q32.32  
C;Function:  
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine  
A;Pathway: signal transduction pathways regulating various processes including insulin a  
e production  
C;Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein  
C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogene  
F;4-106/Domain: pleckstrin repeat homology <PLK>  
F;148-408/Domain: protein kinase homology <KIN>  
F;156-164/Region: protein kinase ATP-binding motif  
F;179/Active site: Lys #status predicted  
F;308/Binding site: phosphate (Thr) (covalent) (by phosphoinositide-dependent protein ki  
F;473/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status experime

Query Match 99.8%; Score 2544; DB 1; Length 480;  
Best Local Similarity 99.8%; Pred. No. 1.9e-101;  
Matches 479; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSDVAIVKEGHLKRGGEYIKTWPRYFLKNDGTFIGYKRPQDVDDREAPLNFSVAQC 60  
Db 1 MSDVAIVKEGHLKRGGEYIKTWPRYFLKNDGTFIGYKRPQDVDDREAPLNFSVAQC 60

Qy 61 QLMKTERPRNTFIIRCLQWTTVIERTFHVETPEEREETTAIQTVADGLKKQEEEMDF 120  
Db 61 QLMKTERPRNTFIIRCLQWTTVIERTFHVETPEEREETTAIQTVADGLKKQEEEMDF 120

Qy 121 RSGSPDSNGABEVSIAKPKHRTVWNEFEYILKLGKTFGKVILVKEKATGRYYAMKI 180  
Db 121 RSGSPDSNGABEVSIAKPKHRTVWNEFEYILKLGKTFGKVILVKEKATGRYYAMKI 180

Qy 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFTQTHDRLCFVMEYANGGELFPHLS 240  
Db 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFTQTHDRLCFVMEYANGGELFPHLS 240

Qy 241 RERVSEDRARFYGAIEVSALDYLHSEKNVYVYRDLENLMDKDGHIKITDFGLCKEGI 300  
Db 241 RERVSEDRARFYGAIEVSALDYLHSEKNVYVYRDLENLMDKDGHIKITDFGLCKEGI 300

Qy 301 KDGATMTKTCGTPPEYLAPEVLENDYGRAVDWGLGVVYEMMCGRLPFYVQDHEKLFEL 360  
Db 301 KDGATMTKTCGTPPEYLAPEVLENDYGRAVDWGLGVVYEMMCGRLPFYVQDHEKLFEL 360

Qy 361 ILMEIEIRPRTLGPPEAKSLLSGLLKDPKQRLGGGSDAKEIMQHRFFAGIVWQHVYEKK 420  
Db 361 ILMEIEIRPRTLGPPEAKSLLSGLLKDPKQRLGGGSDAKEIMQHRFFAGIVWQHVYEKK 420

Qy 421 LSPPFKQVTSSETDTRFYDEEFTAQMITITPPQDDSMCEVDSERRRPHFPQFSYASGTA 480  
Db 421 LSPPFKQVTSSETDTRFYDEEFTAQMITITPPQDDSMCEVDSERRRPHFPQFSYASGTA 480

RESULT 2  
S33364  
protein kinase (EC 2.7.1.37) akt1 [similarity] - mouse  
N;Alternate names: protein kinase B alpha; RAC-PK-alpha;  
C;Species: Mus musculus (house mouse)  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 16-Aug-2004  
C;Accession: S33364  
R;Bellacosa, A.; Franke, T.F.; Gonzalez-Portal, M.E.; Datta, K.; Taguchi, T.; Gardner, J  
Oncogene 8, 745-754, 1993  
A;Title: Structure, expression and chromosomal mapping of c-akt: relationship to v-akt a  
A;Reference number: S33364; MUID:93173519; PMID:8437858  
A;Accession: S33364  
A;Status: preliminary  
A;Molecule type: mRNA

A;Residues: 1-480 <BEL>  
A;Cross-references: UNIPROT:P31750; EMBL:X65687; NID:g287806; PIDN:CAA46620.1; PID:g2878  
C;Genetics:  
A;Gene: MGI:Akt  
A;Cross-references: MGI:87986  
A;Map position: 12  
C;Function:  
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin  
A;Pathway: signal transduction pathways regulating various processes  
C;Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein  
C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogene  
F;4-106/Domain: pleckstrin repeat homology <PLK>  
F;148-408/Domain: protein kinase homology <KIN>  
F;156-164/Region: protein kinase ATP-binding motif  
F;179/Active site: Lys #status predicted  
F;308/Binding site: phosphate (Thr) (covalent) (by phosphoinositide-dependent protein ki  
F;473/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predicte

Query Match 98.4%; Score 2509; DB 1; Length 480;  
Best Local Similarity 98.3%; Pred. No. 5.9e-100;  
Matches 472; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MSDVAIVKEGHLKRGGEYIKTWPRYFLKNDGTFIGYKRPQDVDDREAPLNFSVAQC 60  
Db 1 MNDVAIVKEGHLKRGGEYIKTWPRYFLKNDGTFIGYKRPQDVDDQRESPLNFSVAQC 60

Qy 61 QLMKTERPRNTFIIRCLQWTTVIERTFHVETPEEREETTAIQTVADGLKKQEEEMDF 120  
Db 61 QLMKTERPRNTFIIRCLQWTTVIERTFHVETPEEREETTAIQTVADGLKKQEEETWDF 120

Qy 121 RSGSPDSNGABEVSIAKPKHRTVWNEFEYILKLGKTFGKVILVKEKATGRYYAMKI 180  
Db 121 RSGSPDSNGABEVSIAKPKHRTVWNEFEYILKLGKTFGKVILVKEKATGRYYAMKI 180

Qy 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFTQTHDRLCFVMEYANGGELFPHLS 240  
Db 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFTQTHDRLCFVMEYANGGELFPHLS 240

Qy 241 RERVSEDRARFYGAIEVSALDYLHSEKNVYVYRDLENLMDKDGHIKITDFGLCKEGI 300  
Db 241 RERVSEDRARFYGAIEVSALDYLHSEKNVYVYRDLENLMDKDGHIKITDFGLCKEGI 300

Qy 301 KDGATMTKTCGTPPEYLAPEVLENDYGRAVDWGLGVVYEMMCGRLPFYVQDHEKLFEL 360  
Db 301 KDGATMTKTCGTPPEYLAPEVLENDYGRAVDWGLGVVYEMMCGRLPFYVQDHEKLFEL 360

Qy 361 ILMEIEIRPRTLGPPEAKSLLSGLLKDPKQRLGGGSDAKEIMQHRFFAGIVWQHVYEKK 420  
Db 361 ILMEIEIRPRTLGPPEAKSLLSGLLKDPKQRLGGGSDAKEIMQHRFFAGIVWQHVYEKK 420

Qy 421 LSPPFKQVTSSETDTRFYDEEFTAQMITITPPQDDSMCEVDSERRRPHFPQFSYASGTA 480  
Db 421 LSPPFKQVTSSETDTRFYDEEFTAQMITITPPQDDSMCEVDSERRRPHFPQFSYASGTA 480

RESULT 3  
A40831  
gag-akt polyprotein - AKT8 murine leukemia virus  
N;Contains: amino end of core protein p30; core protein p15; inner coat protein p12; kin  
C;Species: AKT8 murine leukemia virus  
C;Date: 12-Feb-1993 #sequence\_revision 12-May-1994 #text\_change 16-Aug-2004  
C;Accession: A40831; B40831  
R;Bellacosa, A.; Testa, J.R.; Staal, S.P.; Tsichlis, P.N.  
Science 254, 274-277, 1991  
A;Title: A retroviral oncogene, akt, encoding a serine-threonine kinase containing an SH  
A;Reference number: A40831; MUID:92022574; PMID:1833819  
A;Accession: A40831  
A;Molecule type: DNA  
A;Residues: 1-262 <BEL>  
A;Cross-references: GB:M80675  
A;Accession: B40831  
A;Molecule type: DNA  
A;Residues: 262-763 <BE2>

A;Cross-references: GB:M80675  
C;Genetics:  
A;Gene: gag-akt  
C;Superfamily: pleckstrin repeat homology; protein kinase homology  
C;Keywords: ATP; core protein; glycoprotein; oncogene; phosphoprotein; phosphotransferase  
F;1-129/Product: core protein p15 #status predicted <CP1>  
F;130-214/Product: inner coat protein p12 #status predicted <CP2>  
F;284-763/Product: kinase-related transforming protein akt #status predicted <AKT>  
F;287-389/Domain: pleckstrin repeat homology <PLK>  
F;431-691/Domain: protein kinase homology <KIN>  
F;439-447/Region: protein kinase ATP-binding motif  
F;255-337/Binding site: carbohydrate (Aen) (covalent) #status predicted  
F;462/Active site: Lys #status predicted  
F;609/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 98.4%; Score 2509; DB 1; Length 763;  
Best Local Similarity 98.3%; Pred. No. 8.8e-100;  
Matches 472; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MSDVAIVKEGWLHKGGEYIKTRPRYFLKNDGTFIGYKERPDQVQDQREAPLNFSVAQC 60  
Db 284 MNDVAIVKEGWLHKGGEYIKTRPRYFLKNDGTFIGYKERPDQVQDQREAPLNFSVAQC 343

Qy 61 QLMKTERPRNPTFIIRCLQMTTIVERTPHVETPEREETWTTAIQTVDGLKKQEEEMDF 120  
Db 344 QLMKTERPRNPTFIIRCLQMTTIVERTPHVETPEREETWTTAIQTVDGLKKQEEEMDF 403

Qy 121 RSGSPDSNGSGAEEMVSLAKPKHRTVMNEFYLLKLGKGTGKVLVKEKATGRYYAMKI 180  
Db 404 RSGSPDSNGSGAEEMVSLAKPKHRTVMNEFYLLKLGKGTGKVLVKEKATGRYYAMKI 463

Qy 181 LKKEVIVAKDEVATHTLNVRVQLNSRHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLS 240  
Db 464 LKKEVIVAKDEVATHTLNVRVQLNSRHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLS 523

Qy 241 RERVSEDRARFYGAIEVSALDYLHSEKNVYVRDLKLENMLDKDGHIKITDPLGCKEGI 300  
Db 524 RERVSEDRARFYGAIEVSALDYLHSEKNVYVRDLKLENMLDKDGHIKITDPLGCKEGI 583

Qy 301 KDGATMTKTCGTPPYLAPEVLENDYGRAVDWGLGVVYEMWCGRLPFYVQDHEKLFEL 360  
Db 584 KDGATMTKTCGTPPYLAPEVLENDYGRAVDWGLGVVYEMWCGRLPFYVQDHEKLFEL 643

Qy 361 ILMEIEIRPRTLGPPEAKSLLSGLLKDPKQRLGGGSEDAKEIMQHRFPAGIVWQHVYEKK 420  
Db 644 ILMEIEIRPRTLGPPEAKSLLSGLLKDPKQRLGGGSEDAKEIMQHRFPAGIVWQHVYEKK 703

Qy 421 LSPFPKQVTSSETDTRYFDEEFTAQMITITPPDQDDSMCEVDSERRRPHFPQFSYSASGTA 480  
Db 704 LSPFPKQVTSSETDTRYFDEEFTAQMITITPPDQDDSMCEVDSERRRPHFPQFSYSASGTA 763

RESULT 4  
JC2437  
protein kinase (EC 2.7.1.37) akt1 [validated] - rat  
N;Alternate names: protein kinase B alpha; RAC-PK-alpha; serine/threonine-specific prote  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 31-Mar-2001 #sequence\_revision 31-Mar-2001 #text\_change 16-Aug-2004  
A;Accession: JC2437  
R;Konishi, H.; Shinomura, T.; Kuroda, S.; Ono, Y.; Kikkawa, U.  
Biochem. Biophys. Res. Commun. 205, 817-825, 1994  
A;Title: Molecular cloning of rat RAC protein kinase alpha and beta and their associati  
A;Reference number: JC2437; MUID:95091823; PMID:7999118  
A;Accession: JC2437  
A;Molecule type: mRNA  
A;Residues: 1-480 <CON>  
A;Cross-references: UNIPROT:P47196; DBJ:D30040; NID:G485402; PIDN:BAA06279.1; PID:G4854  
A;Experimental source: testis  
C;Function:  
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin  
A;Pathway: signal transduction pathways regulating various processes  
C;Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein  
C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogene

F;4-106/Domain: pleckstrin repeat homology <PLK>  
F;148-408/Domain: protein kinase homology <KIN>  
F;156-164/Region: protein kinase ATP-binding motif  
F;179/Active site: Lys #status predicted  
F;308/Binding site: phosphate (Thr) (covalent) (by phosphoinositide-dependent protein ki  
F;473/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predicte

Query Match 98.3%; Score 2507; DB 1; Length 480;  
Best Local Similarity 98.1%; Pred. No. 7.1e-100;  
Matches 471; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MSDVAIVKEGWLHKGGEYIKTRPRYFLKNDGTFIGYKERPDQVQDQREAPLNFSVAQC 60  
Db 1 MNDVAIVKEGWLHKGGEYIKTRPRYFLKNDGTFIGYKERPDQVQDQREAPLNFSVAQC 60

Qy 61 QLMKTERPRNPTFIIRCLQMTTIVERTPHVETPEREETWTTAIQTVDGLKKQEEEMDF 120  
Db 61 QLMKTERPRNPTFIIRCLQMTTIVERTPHVETPEREETWTTAIQTVDGLKKQEEEMDF 120

Qy 121 RSGSPDSNGSGAEEMVSLAKPKHRTVMNEFYLLKLGKGTGKVLVKEKATGRYYAMKI 180  
Db 121 RSGSPDSNGSGAEEMVSLAKPKHRTVMNEFYLLKLGKGTGKVLVKEKATGRYYAMKI 180

Qy 181 LKKEVIVAKDEVATHTLNVRVQLNSRHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLS 240  
Db 181 LKKEVIVAKDEVATHTLNVRVQLNSRHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLS 240

Qy 241 RERVSEDRARFYGAIEVSALDYLHSEKNVYVRDLKLENMLDKDGHIKITDPLGCKEGI 300  
Db 241 RERVSEDRARFYGAIEVSALDYLHSEKNVYVRDLKLENMLDKDGHIKITDPLGCKEGI 300

Qy 301 KDGATMTKTCGTPPYLAPEVLENDYGRAVDWGLGVVYEMWCGRLPFYVQDHEKLFEL 360  
Db 301 KDGATMTKTCGTPPYLAPEVLENDYGRAVDWGLGVVYEMWCGRLPFYVQDHEKLFEL 360

Qy 361 ILMEIEIRPRTLGPPEAKSLLSGLLKDPKQRLGGGSEDAKEIMQHRFPAGIVWQHVYEKK 420  
Db 361 ILMEIEIRPRTLGPPEAKSLLSGLLKDPKQRLGGGSEDAKEIMQHRFPAGIVWQHVYEKK 420

Qy 421 LSPFPKQVTSSETDTRYFDEEFTAQMITITPPDQDDSMCEVDSERRRPHFPQFSYSASGTA 480  
Db 421 LSPFPKQVTSSETDTRYFDEEFTAQMITITPPDQDDSMCEVDSERRRPHFPQFSYSASGTA 480

RESULT 5  
S62117  
protein kinase (EC 2.7.1.37) akt1 [similarity] - bovine  
N;Alternate names: protein kinase B alpha; RAC-PK-alpha; serine/threonine-specific prote  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 16-Aug-2004  
C;Accession: S62117; S24423; S17999; S15714; S36388  
R;Coffer, P.J.; Woodgett, J.R.  
submitted to the EMBL Data Library, December 1991  
A;Reference number: S62117  
A;Accession: S62117  
A;Molecule type: mRNA  
A;Residues: 1-480 <COF>  
A;Cross-references: UNIPROT:Q01314; EMBL:X61036; NID:G630; PIDN:CAA43371.1; PID:G631  
A;Note: this is a revision to the sequence from reference S17999  
R;Coffer, P.J.; Woodgett, J.R.  
Eur. J. Biochem. 205, 1217, 1992  
A;Reference number: S24423; MUID:92249329; PMID:1533586  
A;Contents: erratum  
A;Accession: S24423  
A;Status: nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 70-78, N', 80-145 <COW>  
A;Cross-references: EMBL:X61036  
A;Note: this is a revision to the sequence from reference S17999  
R;Coffer, P.J.; Woodgett, J.R.  
Eur. J. Biochem. 201 475-481, 1991  
A;Title: Molecular cloning and characterisation of a novel putative protein-serine kinas  
A;Reference number: S17999; MUID:92037600; PMID:1718748



F;181/Active site: Lys #status predicted

Query Match	82.9%	Score 2113.5;	DB 1;	Length 481;
Best Local Similarity	81.4%;	Pred. NO. 3.4e-83;		
Matches 390;	Conservative	52;	Mismatches 34;	Indels 3;
				Gaps 2;

	Qy	1	MSDVAIVKEGVLHKRGYIITWPRPYFLLLKNDGTFIGYKERPDVDQREAPLNNFSVAQC	60
	Dd	1	MNEVSVIKEGLHKGRIYIITWPRPYFLLLKSDGSFIGYKERPEADQTLPPLNNSVAEC	60
	Qy	61	QLMKTERPNTFTIRCLQWTTVIERTFPHVETPEREEWTTAITQTVADGLKKQ--EBEEM	118
	Dd	61	QLMKTERPNTFVIRCLQWTTVIERTFPHVDSPPEREEWPAIQNVANSCLKQRGGEDAM	120
	Qy	119	DFRSGSPSDNSGAEMEVSIAKPXHRVTMMNEFEYLKLLGKGTFGKVILVREKATGRYYAM	178
	Dd	121	DYKCGSPSDSTSEMMEVAVS KARAKVTMNFDFYLLKLGKTFGKVILVREKATGRYYAM	180
	Qy	179	KILKKEVIIVAKDEVAHTLTENRVLONSRHPFLTALKYSFOTHDRLCFMVEYANGELFFH	238
	Dd	181	KILRKVEIIIAKDEVAHTVTSRVLQNRHPFLTALKYAFQTHDRLCFMVEYANGEDLFFH	240
	Qy	239	LSRERVFESDRARFYGAEIVSALDYLSHEKNVVYRDIKLENMLDKDGHIKITDIFGLCKE	298
	Dd	241	LSRERVFTEDRARFYGAEIVSALEYLHS--TDVVYRDIKLENLMLDKDGHIKITDIFGLSKE	299
	Qy	299	GIKDGA TMKTCFCTPEYLAPEVL EDNDNYGRAVDWMGLGVVMYEMMCGRLLPFYNODHKLF	358
	Dd	300	GISDGA TMKTCFCTPEYLAPEVL EDNDNYGRAVDWMGLGVVMYEMMCGRLLPFYNODHERLF	359
	Qy	359	ELIIMBEIRPRTLGP EAKSL LSKLLKKDPKORLCGGSSEDAKETWOHRFPAGI VQWVYE	418
	Dd	360	ELIIMBEIRPRTLGP EAKSLLAGULLKKDPKORLCGGSFDAKEVWEHRFFLSINQDWVQ	419
	Qy	419	KKLSPPPKPOVTSTDTTRYDFDEFTAQM IITTPPDQDDSMCEVDSERRPHFPQSFSAS	477
	Dd	420	KXLPLPPKPOVTSEVDTRYDFDEFTAQSIITTPPDRYDSLGSLELDORTFFPQPFSYSAS	478

RESULT 8

A59380

protein kinase (EC 2.7.1.37) akt3 long splice form [similarity] - human  
N;Alternate names: protein kinase B gamma; RAC-PK-gamma; serine/threonine-specific protei  
C;Species: Homo sapiens (man)  
C;Date: 31-Mar-2001 #sequence\_revision 31-Mar-2001 #text\_change 16-Aug-2004  
C;Accession: A59380; A59379  
R;Brodbbeck, D.; Cron, P.; Hemmings, B. A.  
J. Biol. Chem. 274, 9133-9136, 1999  
A;Title: A human protein kinase Bgamma with regulatory phosphorylation sites in the acti  
A;Reference number: A59380; MUID:59194749; PMID:10092583  
A;Accession: A59380  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-479 <BRO>  
A;Cross-references: UNIPROT:Q9Y243; GB:AAD29089; NID:94757579; PIDN:AAD29089.1  
R;Masuue, S.; Haefner, B.; Wesselsink, J. J.; Hoefnagel, E.; Mortier, E.; Verhasselt, P.;  
Eur. J. Biochem. 265, 353-360, 1999  
A;Title: Molecular cloning, expression and characterization of the human serine/threonin  
A;Reference number: A59379; MUID:99421751; PMID:10491192  
A;Accession: A59379  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-479 <MAS>  
A;Cross-references: GB:CAB53537; NID:95804886; PIDN:CAB53537.1  
C;Genetics:  
A;Gene: GDB:AKT3; PRXBG; PRXBG; RAC-gamma  
A;Cross-references: GDB:9954867  
A;Map position: 1q44-1q44  
C;Function:  
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin  
A;Pathway: signal transduction pathways regulating various processes  
C;Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein  
C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase proto-oncogene

F;7-108/Domain: pleckstrin repeat homology <PIK>  
F;149-408/Domain: protein kinase homology <KIN>  
F;157-165/Region: protein kinase ATP-binding motif  
F;177/Active site: Lys #status predicted  
F;305/Binding site: phosphate (Thr) (covalent)  
F;404/Binding site: phosphate (Ser) (covalent)

Query Match 82.6%; Score 2105.5; DB 1; Length 479;  
Best Local Similarity 82.7%; Pred. No. 7.4e-83;  
Matches 397; Conservative 36; Mismatches 42; Indels 5; Gaps 4;

Qy	1	MSDVAIVKSGWLHKRGYEIKTWPRPVFLLLKQDGTFFICYKERPODVOREAPLNNSFVAQC	60
Db	1	MSDVTIVKSGWQKRGYEIKWPRPVFLLLKQDGTGSGFICYKPKQDVB-LPYPLNNSFVAKC	59
Qy	61	QLMKTRPRNPNTFIIRCLQWTTVIBRTHEVETPEEREEMTTALQTADVADGKKQEBEEMDF	120
Db	60	QLMKTRPRNPNTFIIRCLQWTTVIBRTHEVETPEEREEMTTALQAVADRLQREBERMNC	119
Qy	121	RGSPSDNSGAEEMEYSLAKPHRVTMNFEYFLKLLGKGTFGKVILVYKEKATGRYYAMKI	180
Db	120	SPTSQIDNIGEEEMDASTHHK-RKTMNDFDYLKLLGKGTFGKVILVREKASGYAMKI	178
Qy	181	LKEEIVAVKDEVAHTLTENRVLONSHBPLTALKYSFOTHRDLRCFVMEYANGELPFHLS	240
Db	179	LKEEVIIAKDEVAHTLTESRVLKNTBPLTSLUKYSFQTKDRLCFVMEYVNGELPFHLS	238
Qy	241	REVFSEDRARFYGAEIVSALDYLHSEKNVYRDCLKLENMLDKDGHIKITDFGLCKEGI	300
Db	239	REVFSEDRTRFYGAEIVSALDYLHSGK-IVYRDCLKLENMLDKDGHIKITDFGLCKEGI	297
Qy	301	KDGAATWKTFCGTPYEYLAPEVLENDYGRAVDMWGLGVMEYMMCGRLPFYNQDHEKLFEL	360
Db	298	TDAATWKTFCGTPYEYLAPEVLENDYGRAVDMWGLGVMEYMMCGRLPFYNQDHEKLFEL	357
Qy	361	ILMEEIRFPRTLGLPEAKSLLSGLLKDKPKORLGGGSEDAKEIMOHFFPAGIVQHVVEKK	420
Db	358	ILMEDIKFRTLSSDAKSLLSGLLIKDPKNRGLGGGPDDAKEIMRHSFFSGVNWQDYDKK	417
Qy	421	LSPPPKPQVTSZTDTRYFDEEFTAQMITTPPDQ--DDSMCEVDSERRPHFPQFSYSASG	478
Db	418	LVPFPKPVTSZTDTRYFDEEFTAQMITTPPKYDGEDGMDCMDSERRPHFPQFSYSASG	477

RESULT 9  
T17287

protein kinase (EC 2.7.1.37) akt3 short splice form - human  
N;Alternate names: protein kinase B gamma; RAC-PK-gamma; serine/threonine-speci  
C;Species: Homo sapiens (man)  
C;Date: 31-Mar-2001 #sequence\_revision 31-Mar-2001 #text\_change 16-Aug-2004  
C;Accession: T1287  
R;Pouscka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.  
submitted to the Protein Sequence Database, September 1999  
A;Reference number: Z18723

A;Accession: T17287  
A;Molecule type: mRNA  
A;Residues: 1-462 <FOU>  
A;Cross-references: EMBL:AL117525; GB:CA855977; NID:55912043; PIDN:CA855977.1  
A;Experimental source: adult testis; clone DKFp434N0250  
R;Nakatani, K.; Thompson, D.A.; Barthel, A.; Sakaue, H.; Liu, W.; Weigel, R.J.;  
J. Biol. Chem. 274, 21528-21532, 1999  
A;Title: Up-regulation of Akt3 in estrogen receptor-deficient breast cancers and  
A;Reference number: A64199; PMID:10419456

A;Gene: GDB:AKT3  
A;Cross-references: GDB:9954867  
A;Map position: 1q44-1q44

A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl  
A;Pathway: signal transduction pathways regulating various processes  
C;Function:  
A;Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology;  
A;map\_position: 1q44-1q45

A; Gene: GDB:AA13; FASG; FASBG; RAC-9  
A; Cross-references: GDB:9954867  
A; Map position: 1q44-1q44  
C; Function:

A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin A;Pathway: signal transduction pathways regulating various processes C;Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogene





Db 107 VKEGMLKRCGEHIKNWRQRFVLHSDGRLMGVRSKP--ADSASTPSPDFLLANNFVRGCQ 164  
Qy 62 LMKTERPRNPFTIIRCLQWTTVIERTFHVETPBEREWTTAIQTVDGLKFKQBESEMDFR 121  
Db 165 IMTVDRPKPFTFIIRGLQWTTVIERTFHVETPBEREWTTAIQTVDGLKFKQBESEMDFR 221  
Qy 122 SGSPSDNSGAEMEV-SLAKPK-----HRVTNNEPEYLKLLCKGTGFK 163  
Db 222 --TFSEQTDMDTVDMAITAEDELSEQFSVQTTNCSGKVKVTLENFEFLKVLGKGTGFK 279  
Qy 164 VILVKEKATGRYYAMKILKKEVIVAKDEVAHTLNTENRVLQNSRHPFTALYSPQTHDRL 223  
Db 280 VILCREKATAKLYAIKILKKEVILQKDEVAHTLNTENRVLQNSRHPFTALYSPQTHDRL 339  
Qy 224 CFVMEYANGELFPHLSRVSFSDRARFYGAETVSALDYHLSKKNVYRDLKLENLMD 283  
Db 340 CFVQYVNGGELFWHLHERIFTEDRTRFYGAETVSALDYHLSQ-GIIYRDLKLENLMD 398  
Qy 284 KDGHIKTDFGLCKEGIKDGMATKTCGTPEYLAPEVLDDNDYGRAVDWGLGVVMEYM 343  
Db 399 KDGHIKVDGFLCKEDITYGRTTKTFCGTPEYLAPEVLDDNDYQAVDWMGTGVVMEYM 458  
Qy 344 CGRLPFYNQDHEKLFELILMBEIRFPRTLGPPEAKSLLSGLLKDPKORLGGSGSEDAKEIM 403  
Db 459 CGRLPFYNRHDVLFLLVEEVKFRNITDEAKNLLAGLLAKDPKRLGGGKDDVKEIQ 518  
Qy 404 QHRRFAGIVQHVVEKLSPPPKQVTSQVSETDTRYFDEEFTAQMITITPPDODDSMECVDS 463  
Db 519 AHPFFASINWTDVLKIKPPPKQVTSQVSETDTRYFDEEFTAQMITITPPDODDSMECVDS 578  
Qy 464 ERHPFPQFSV-----SASGTA 480  
Db 579 E--PLFPQFSYQGMMASTLGTGS 598

RESULT 12  
T43232  
Protein kinase (EC 2.7.1.37) akt-1 splice form b [similarity] - Caenorhabditis elegans  
N;Alternate names: PKB; protein kinase B  
C;Species: Caenorhabditis elegans  
C;Date: 31-Mar-2001 #sequence\_revision 31-Mar-2001 #text\_change 16-Aug-2004  
C;Accession: T43232; T19222  
R;Paradis, S.; Ruvkun, G.  
Genes Dev. 12, 2488-2498, 1998  
A;Title: Caenorhabditis elegans Akt/PKB transduces insulin receptor-like signals from AG  
A;Reference number: 222355; MUID:98382502; PMID:9716402  
A;Accession: T43232  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-546 <PAR>  
A;Cross-references: UNIPROT:Q17942; EMBL:AF072380; NID:g3694830; PIDN:AAC62467.1; PID:g3694830  
R;McMurray, A.  
submitted to the EMBL Data Library, June 1996  
A;Reference number: 219092  
A;Accession: T19222  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-546 <WIL>  
A;Cross-references: EMBL:Z73969; PIDN:CAA98238.1; GSPDB:GNO0023; CESP:C12D8.10b  
A;Experimental source: clone C12D8  
C;Genetics:  
A;Gene: akt-1; C12D8.10  
A;Map position: 5  
A;Introns: 35/2; 71/3; 134/3; 188/3; 254/3; 323/3; 366/3; 487/3  
C;Function:  
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine  
A;Pathway: signal transduction pathways regulating metabolism, development, and longevity  
C;Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein  
C;Keywords: alternative splicing; ATP; autophosphorylation; phosphoprotein; phosphotrans  
F;14-116/Domain: pleckstrin repeat homology <PLK>  
F;191-455/Domain: protein kinase homology <KIN>  
F;199-207/Region: protein kinase ATP-binding motif  
F;222/Active site: Lys #status predicted

F;355/Binding site: phosphate (Thr) (covalent) #status predicted  
F;522/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predicted

Query Match 58.5%; Score 1490.5; DB 1; Length 546;  
Best Local Similarity 55.6%; Pred. No. 9.8e-57;  
Matches 283; Conservative 78; Mismatches 107; Indels 41; Gaps 7;

Qy 6 IVKEGMLKRCGEYIKTWPRFYLLKNDGTGFIYKERQDVQDREAPLNNFSAVQCOLMKT 65  
Db 16 WTIEGMLHKGEHIRNWRPFYFMIDGALGLFRAKKEGQFPPEPLNDFMIKDAATMLF 75  
Qy 66 ERBPNTFIIRCLQWTTVIERTFHVETPBEREWTTAIQTVDGLK-----KQBE---- 115  
Db 76 EKRPANFWRCLOWTTVIERTFVAESAERQRIHAIESISKYKGTNANPQBELMETN 135  
Qy 116 -----EEMDFRS-----GSPSDNSG-----AEEMEVSILAKPKHRVTNNEPEY 152  
Db 136 QQPKIDEDSEFAGAAHAIMGOPSSGCHDNCSDIPRSMISIAADTSEAAKRDKITMEDPDF 195  
Qy 153 LKLLGKGTGKVLIVKEKATGRYYAMKILKEVIVAKDEVAHTLNTENRVLQNSRHPFLTA 212  
Db 196 LKVLGKGTGKVLIVKEKATGRYYAMKILKEVIVAKDEVAHTLNTENRVLQNSRHPFLTA 255  
Qy 213 LKYSFQTHDRLCFVMEYANGELFFHLRS-----RVFSEDRARFYGAETVSALDYHLS 267  
Db 256 LKYSFQTHDRLCFVMEYANGELFFHLRS-----RVFSEDRARFYGAETVSALDYHLS 314  
Qy 268 KNVYRDLKLENLMDKDGHIKTDFGLCKEGIKDGMATKTCGTPEYLAPEVLDDNDY 327  
Db 315 NSIVYRDLKLENLMDKDGHIKTDFGLCKEGIKDGMATKTCGTPEYLAPEVLDDNDY 374  
Qy 328 RAVDWGLGVVMEYEMCGRLPFYNQDHEKLFELILMBEIRFPRTLGPPEAKSLLSGLLK 387  
Db 375 RCVDWGLGVVMEYEMCGRLPFYNQDHEKLFELILMBEIRFPRTLGPPEAKSLLSGLLK 434  
Qy 388 PKORLGGSGSEDAKEIMOHRFPFAGIVQHVVEKLSPPPKQVTSQVSETDTRYFDEEFTAQMI 447  
Db 435 PTQRLGGSGSEDAKEIMOHRFPFAGIVQHVVEKLSPPPKQVTSQVSETDTRYFDEEFTAQMI 494  
Qy 448 TITPPDODDSMECV--SERRPFPQFSY 474  
Db 495 QLTPPSSGALATVDEQEEMQSNFTQFSF 523

RESULT 13  
T43232  
Protein kinase (EC 2.7.1.37) akt-1 splice form a [similarity] - Caenorhabditis elegans  
N;Alternate names: PKB; protein kinase B  
C;Species: Caenorhabditis elegans  
C;Date: 31-Mar-2001 #sequence\_revision 31-Mar-2001 #text\_change 16-Aug-2004  
C;Accession: T43232; T19222  
R;Paradis, S.; Ruvkun, G.  
Genes Dev. 12, 2488-2498, 1998  
A;Title: Caenorhabditis elegans Akt/PKB transduces insulin receptor-like signals from AG  
A;Reference number: 222355; MUID:98382502; PMID:9716402  
A;Accession: T43232  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-541 <PAR>  
A;Cross-references: UNIPROT:Q17941; EMBL:AF072379; NID:g3694828; PIDN:AAC62466.1; PID:g3694828  
R;McMurray, A.  
submitted to the EMBL Data Library, June 1996  
A;Reference number: 219092  
A;Accession: T19222  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-541 <WIL>  
A;Cross-references: EMBL:Z73969; PIDN:CAA98240.1; GSPDB:GNO0023; CESP:C12D8.10a  
A;Experimental source: clone C12D8  
C;Genetics:  
A;Gene: akt-1; C12D8.10  
A;Map position: 5  
A;Introns: 35/2; 71/3; 134/3; 188/3; 254/3; 318/3; 361/3; 482/3



C;Function:

A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine-phosphate

A;Pathway: signal transduction pathways regulating metabolism, development, and longevity

C;Superfamily: RAC serine/threonine-protein kinase, pleckstrin repeat homology; protein

C;Keywords: alternative splicing; ATP; autophosphorylation; phosphoprotein; phosphotransferase

F;114-116/Domain: pleckstrin repeat homology <PH>

F;191-450/Domain: protein kinase homology <KIN>

F;199-207/Region: protein kinase ATP-binding motif

F;222/Active site: Lys #status Predicted

F;350/Binding site: phosphate (Thr) (covalent) #status Predicted

F;517/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status Predicted

Query Match 57.6%; Score 1470; DB 1; Length 541;  
Best Local Similarity 55.4%; Pred. No. 7.2e-56;  
Matches 279; Conservative 75; Mismatches 114; Indels 36; Gaps 6;

Qy	6	IVKEGWLHKGEVYIKTWRRPYFLKNDGTIGYKRPQVDQREAPLNPFSAQCQLMKT	65
Db	16	VVIEGWLHKGEHINRRPRPYFINDGALLGFRAPKPKGQPPPEPLNDFMIDAAATMLF	75
Qy	66	ERRPNTFIIRCLQWTVIERTVETPEERESEWTTAQTAVDGLK-----KQEE-----	115
Db	76	EKRPANFMVRCQLQWTVIERTVETVYAESAEVQRQWHAIESISKYKGTNANPQEEELMETN	135
Qy	116	-----EEMDFRS-----GSPSDNSG-----AEEMEVSLAKPKHRYTNNEFEY	152
Db	136	QQPKIDSESFAGAAHAIMGQPSGGHGNCSIDFRASMISIADTSEAAKDKITMEDDFD	195
Qy	153	LKLLGKTGFKVILVKEKATGRVYAMKILKKEVIVAKDEVAAHTLTENRVLQNSRHPFLTA	212
Db	196	LKVLGKTGFKVILCKEKRTQKLYAIKILKDVIIAREEVAHTLTENRVLQRCCKHPFLTE	255
Qy	213	LKYSFQTHDRLCFWMEYANGGELFFHLRSRVPSEDRARPYGAEIVSALDYLHSEKNVVY	272
Db	256	LKYSFQEQHYLCFWQMPANGELFTVRKCGTSEPRARPYGAEIVLALGYLH-RCDIVY	314
Qy	273	RDALKLENMLDKDGHKITIDFGCKEGIKDGAATMTCFGTPPEYLAPEVLEDNDYGRAVDW	332
Db	315	RDMLKENLLDKDGHKIADFGLCKEEISFGDKTSTFCGTPPEYLAPEVLDDHDYGRCDW	374
Qy	333	WGLGVVYVYEMWCGRLPPYNODHEKLELILMSEIRPRTLGPPEAKSILLGLLKQDPKQL	392
Db	375	WGVGVVYVYEMWCGRLPPYKDXHNLKLELIMAGDLRFPFKLSQSEARTLLTGLLYKDPQRL	434
Qy	393	GGGSEDAKEIMQRFAGIVQWQVYEKKLSPPPKPOVTSBTDTRYDDEEFTAQMITTPP	452
Db	435	GGGPEDALEICRADFPFTVDWEATYRKEIEPPYKPNVQSETDTSYFDNETSPVOLITPP	494
Qy	453	QDDDSMECVD--SERRPHFPQFSY 474	
Db	495	SRSGALATVDEOEMOSNFTQFSF 518	

RESULT 14  
T21523  
protein kinase (EC 2.7.1.37) akt-2 long splice form [similarity] - Caenorhabditis elegans  
N;Alternate names: PKB; protein kinase B  
C;Species: Caenorhabditis elegans  
C;Date: 31-Mar-2001 #sequence\_revision 31-Mar-2001 #text\_change 16-Aug-2004  
C;Accession: T21523; T23878

submitted to the EMBL Data Library, September 1998

A;Reference number: Z19434  
A;Accession: T21523  
A;Status: translated from GB/EMBL/DDJ  
A;Molecule type: DNA  
A;Residues: 1-528 <WIL>  
A;Cross-references: UNIPROT:Q9XGTG; EMBL:AL031621; PIDN:CAA20936.1; GSPDB:GNC00028; CESP:  
R;McMurray, A.  
submitted to the EMBL Data Library, March 1997

A;Reference number: Z19812  
A;Accession: T23878

A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-528 <W12>  
A:Cross-references: EMBL:Z92837; PIDN:CAB07403.1; GSPDB:GN00028; CESP:F28H6.1  
A:Experimental source: clone R03E1  
C:Genetics:  
A:Gene: akt-2; CESP:F28H6.1  
A:Map position: X  
A:Introns: 32/2; 68/3; 135/3; 175/3; 241/3; 285/2; 305/3; 348/3; 469/3  
C:Function:  
A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine-phosphate  
A:Pathway: signal transduction pathways regulating metabolism, development, and longevity  
C:Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein  
C:Keywords: alternative splicing; ATP; autophosphorylation; phosphoprotein; phosphotransferase  
F:11-113/Domain: pleckstrin repeat homology <P1K>  
F:178-437/Domain: protein kinase homology <KIN>  
F:188-194/Region: protein kinase ATP-binding motif  
F:209/Active site: Lys #status predicted  
F:337/Binding site: phosphate (Thr) (covalent) #status predicted  
F:505/Binding site: phosphate (Ser) (covalent) #status predicted

	Query Match	54.5%;	Score 1390.5;	DB 1;	Length 528;
	Best Local Similarity	52.7%;	Pred. No. 1.7e-52;		
	Matches 265;	Conservative 87;	Mismatches 118;	Indels 33;	Gaps 7;
Qy	6	IVKEGWLHKRGYIIKTRPRYFLLNKDGTFIGYKERPDVDREAPLNPNFSAQCQLMKT	65		
Db	13	IVIESWLHKKGSHIRNWRPRYFILPRDGLLGFSPKPKEDQPLPEPLNNFMIRDAATVCL	72		
Qy	66	ERPRNTPIIRCLQWTVIERTFHVETPEEREWTVAIQTVAD-----GLKKQBESE	117		
Db	73	DKPRENMPIVRCLQWTVIERTFYADSADFQWMIQAVSSHNLKENAGNTSMQBED	132		
Qy	118	MDFRSGSPSDNSGA-----EEMEVSIAKP-----KHRVTWNEPEYLLKLLKG	159		
Db	133	---TNGNPSGESDVNDATSTRSDNDFESIVMNIIDPEEVPKNTVTMDDFDLKVLGG	189		
Qy	160	TFGKVLVKEKATRGYYAMKILKKEVIVAKDEVAHTLTENRVLQNSRHPFITALKYSPT	219		
Db	190	TFGKVLCKREKSDKLYAIKIRKENMVDVRSEVAHTLTENRVLYACVHPFLLTKYSQA	249		
Qy	220	HDRLCFVMEYANGGELFHLSERFVSEDRARVFGAEIVSALDYLHSEKNVYVRDLKLEN	279		
Db	250	QYHICFVMEFANGGELFTHLQCKTSEARTIRYGSIIIALGYLH-HRNIVYRDMKLEN	308		
Qy	280	LMLDKDGIKITDFGLCKEGIKDGAATMTCFCGTFEYLAPEVLEDNDYGRAVDMWGLGVVM	339		
Db	309	LLLDRDGHIKITDFGLCKEEIKYGDNTSTFCGTFEYLAPEVIEDIDYDRSVDMWGVVM	368		
Qy	340	YEMMCGRLPFYQNDHEKLPFLILMEIRIPRTTLPENAKSLSLGLKKDPKORLGGGSDA	399		
Db	369	YEMMCGRLPFSKAKNGKLPFLITCDLQKFNRLSPSAVTLTSLGLLVRVPKRLGAGPDA	428		
Qy	400	KEIMQHRFPAGIVVQHVVEKKLSPPPKPOVTSSTDTRYFDEEFTAQMITITPPDQDSME	459		
Db	429	REVSRAEFKVDVMEATLKEVEPPPKPNVMSTDTSTFFDREFTMPVQLTPPRGEELP	488		
Qy	460	CVDSESR--RPHPQPF-SYASGTT	479		
Db	489	TVDEERLOANFIORASYVYVSGS	511		

RESULT 15  
T43234  
protein kinase (EC 2.7.1.37) akt-2 short splice form [similarity] - Caenorhabditis elegans  
N/Alternate names: PKB; protein kinase B  
C/Species: Caenorhabditis elegans  
C/Date: 31-Mar-2001 #sequence\_revision 31-Mar-2001 #text\_change 16-Aug-2004  
C/Accession: T43234  
R/Paradis, S.; Ruvkun, G.  
Genes Dev. 12, 2488-2498, 1998  
A/Title: Caenorhabditis elegans Akt/PKB transduces insulin receptor-like signals from AGC1 and AGC2 protein kinases through a 14-3-3 dependent mechanism  
A/Reference number: Z22355; MUID:98382502; PMID:9716402

A:Accession: T43234  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-483 <PAR>  
A:Cross-references: UNIPROT:O77145; EMBL:AF072381; NID:g3694832; PIDN:AAC62468.1; PID:g3694832  
C:Genetics:  
A:Gene: akt-2  
C:Function:  
A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin  
A:Pathway: signal transduction pathways regulating metabolism, development, and longevi  
C:Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein  
C:Keywords: alternative splicing; ATP; phosphoprotein; phosphotransferase; serine/threon  
F:11-113/Domain: pleckstrin repeat homology <PLK>  
F:178-437/Domain: protein kinase homology <KIN>  
F:186-194/Region: protein kinase ATP-binding motif  
F:209/Active site: Lys #status predicted  
F:337/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 51.9%; Score 1324; DB 1; Length 483;  
Best Local Similarity 54.1%; Pred. No. 1e-49;  
Matches 249; Conservative 78; Mismatches 103; Indels 30; Gaps 5;

Qy 6 IVKEGWLHKGREYIKTWPRYFLKNDGTFYGYKERPOVDQREAPLNFSVAQCQLMKT 65  
Db 13 IVIESWLHKGGEHINRWRPRYFILFRDGTLLGFSKPKEDQPLPEPLANNFIRDAATVCL 72

Qy 66 ERPRNTFIIRCLQWTTVIERTFHVETPEERBEWTTAQTAD-----GLKKQBEER 117  
Db 73 DKPRPNMFIIVRCLQWTTVIERTFVADSADFRQMITEATQAVSSHNRLENAGNTSMQBED 132

Qy 118 MDRSGSPSDNSGA-----EEMEVSLAKP-----KRVTMNEFEYLKLGKG 159  
Db 133 ---TGNPFGSDVNM DATSTRSDNFESTVMNIDPEEVPKNTVTMDDFDLKVLGQG 189

Qy 160 TFGKVLVKEKATGRYAMKILKKEVIVAKDEVHTLTENRVLQNSRHPFLTALKYSFQT 219  
Db 190 TFGKVLCKREKSSDKLYAKIKRMVVDREVAHTLTENRVLYACVHPFLTLLKYSFQA 249

Qy 220 HDRLCFVMEYANGGELPFHLGRVRFSEDRARFYGAETVSALDYHSEKNVYRDLEN 279  
Db 250 QYHICFVMEFANGGELFTHLQRCCKTFSEARTFYGSEIILALGYLH-HRNIVYRDMKLEN 308

Qy 280 LMLDKDGHIKITDFGLCKEGIKDGATMKTFCGTPYLAPEVLENDYGRAVDWMLGVVM 339  
Db 309 LLLDRDGHIKITDFGLCKEEIKYDKTSTFCGTPYLAPEVIDIDYDRSDWMLGVVM 368

Qy 340 YEMMCGRLPFYNQDHEKLFELIMBEIRFPRTLGLPEAKSLLSGLIKKDPKQRLGGSEDA 399  
Db 369 YEMMCGRLPFSKENGKLFELITTCDLAKFPNRLSPEAVTLLSGLLERYVPKRLGAGPDDA 428

Qy 400 KEIMQHRFFAGIVQHVYVEKLSPPFKQVTSPTDTRYFD 439  
Db 429 REVSRAEFFKDVDEATLRKEVEPPFKPNVMSPTDTSFFD 468

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OM protein - protein search, using sw model

Run on: February 23, 2005, 20:22:18 ; Search time 164 Seconds  
(without alignments)  
1131.982 Million cell updates/sec

Title: US-10-621-485A-1

Perfect score: 2550

Sequence: 1 MSDVAIVKEGWLHKRGYIK.....VDSERRPHQFSYASSTA 480

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

1: geneseqp1980s:\*

2: geneseqp1990s:\*

3: geneseqp2000s:\*

4: geneseqp2001s:\*

5: geneseqp2002s:\*

6: geneseqp2003as:\*

7: geneseqp2003bs:\*

8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2550	100.0	492	6	ABO27207 Human sig
2	2544	99.8	480	2	AAW17972 Human RAC
3	2544	99.8	480	2	AAW18515 Human RAC
4	2544	99.8	480	2	AAW52706 Human AKT
5	2544	99.8	480	2	AAW33999 Human AKT
6	2544	99.8	480	2	ADf77614 Human AKT
7	2544	99.8	480	3	ADf77614 Human AKT
8	2544	99.8	480	4	ADf77614 Human AKT
9	2544	99.8	480	4	ADf77614 Human AKT
10	2544	99.8	480	4	ADf77614 Human AKT
11	2544	99.8	480	5	ADf77614 Human AKT
12	2544	99.8	480	5	ADf77614 Human AKT
13	2544	99.8	480	5	ADf77614 Human AKT
14	2544	99.8	480	6	ADf77614 Human AKT
15	2544	99.8	480	7	ADf77614 Human AKT
16	2544	99.8	480	7	ADf77614 Human AKT
17	2544	99.8	480	8	ADf77614 Human AKT
18	2544	99.8	480	8	ADf77614 Human AKT
19	2544	99.8	480	8	ADf77614 Human AKT
20	2544	99.8	480	8	ADf77614 Human AKT
21	2544	99.8	480	8	ADf77614 Human AKT
22	2544	99.8	480	8	ADf77614 Human AKT
23	2544	99.8	480	8	ADf77614 Human AKT
24	2544	99.8	480	8	ADf77614 Human AKT
25	2544	99.8	480	8	ADf77614 Human AKT

26	2540	99.6	480	2	AAW17984	AAW17984 Human RAC
27	2538	99.5	480	2	AAW17983	AAW17983 Human RAC
28	2534	99.4	480	2	AAW17985	AAW17985 Human RAC
29	2509	98.4	480	3	AAW22223	AAW22223 Wild type
30	2509	98.4	480	5	AAE17784	AAE17784 Mouse Akt
31	2509	98.4	501	2	AAW03452	AAW03452 Mouse v-A
32	2509	98.4	517	8	ADL25357	ADL25357 ARK5 rela
33	2503	98.2	480	7	ADf83507	ADf83507 Rat Prote
34	2494	97.8	480	3	AAW06176	AAW06176 Human hA
35	2493.5	97.8	480	3	AAW03453	AAW03453 Mouse c-A
36	2464	96.6	480	8	ADN71942	ADN71942 Chicken s
37	2161.5	84.8	417	3	AAW22222	AAW22222 Partial w
38	2161.5	84.8	417	5	AAE17783	AAE17783 Human Akt
39	2156.5	84.6	417	8	ADf55980	ADf55980 Human Akt
40	2138.5	83.5	488	8	ABO84895	ABO84895 Murine ca
41	2136.5	83.4	480	4	AAW78019	AAW78019 Human Akt
42	2136.5	83.4	480	4	AAW19997	AAW19997 Human ser
43	2136.5	83.4	480	8	ADG85254	ADG85254 Human Chr
44	2136.5	83.4	481	3	AAW53246	AAW53246 Human Akt
45	2136.5	83.4	481	5	AAW79419	AAW79419 Human pro

## ALIGNMENTS

### RESULT 1

#### ABO27207

ID ABO27207 standard; protein; 492 AA.

XX ABO27207;

AC ABO27207;

DT 10-SEP-2003 (first entry)

DE Human signal transduction pathway component HJBCX80.

XX Human; signal transduction pathway component; gene therapy; cancer;  
 KW neural disorder; immune system disorder; systemic lupus erythematosus;  
 KW rheumatoid arthritis; multiple sclerosis; muscular disorder; sinusitis;  
 KW respiratory disease; nasal vestibulitis; nasal polyp; pulmonary disorder;  
 KW cardiovascular disorder; congenital heart defect; Ebstein's anomaly;  
 KW hypoplastic left heart syndrome; renal disorder; acute kidney failure;  
 KW end-stage renal disease; hyperproliferative disorder; Hodgkin's disease;  
 KW leukemia; inflammatory disease; septic shock; bursitis; appendicitis;  
 KW allergy; asthma; blood related disorder; thrombosis; atherosclerosis;  
 KW myocardial infarction; endocrine disorder; Addison's disease; dysphagia;  
 KW corticosteroid deficiency; reproductive system disorder; dysmenorrhea;  
 KW testicular atrophy; gastrointestinal disorder; irritable bowel syndrome;  
 KW infectious disease; wound healing; epithelial cell proliferation.

XX Homo sapiens.

XX US2003036505-A1.

XX 20-FEB-2003.

PF 20-SEP-2001; 2001US-00955999.

PR 25-SEP-2000; 2000US-0234997P.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Barash SC, Ni J, Ruben SM, Rosen CA, Young PE, Rohrschneider LR;

XX WPI; 2003-492122/46.

DR N-PSDB; ACD44893.

XX New isolated nucleic acids encoding signal transduction pathway component  
 PT polypeptides, useful for diagnosing, treating, and/or preventing  
 PT disorders, such as cancer, infections, cardiovascular and inflammatory  
 PT diseases.

XX Claim 11; Page 270-271; 297pp; English.

XX

CC The invention relates to an isolated nucleic acid molecule. The methods  
 CC and compositions of the present invention are useful for diagnosing,  
 CC treating, preventing and/or prognosing disorders related to the novel  
 CC polypeptides, such as neural disorders, immune system disorders (e.g.  
 CC systemic lupus erythematosus, rheumatoid arthritis, or multiple  
 CC sclerosis), muscular disorders, respiratory diseases (e.g. nasal  
 CC vestibulitis, nasal polyps, or sinusitis), reproductive disorders,  
 CC gastrointestinal disorders, pulmonary disorders, cardiovascular disorders  
 CC (e.g. congenital heart defects, Ebstein's anomaly or hypoplastic left  
 CC heart syndrome), renal disorders (e.g. acute kidney failure, or end-stage  
 CC renal disease), hyperproliferative disorders (e.g. Hodgkin's disease or  
 CC leukaemia), inflammatory diseases (e.g. septic shock, bursitis, or  
 CC appendicitis), allergic reactions and conditions (e.g. asthma), blood  
 CC related disorders (e.g. thrombosis, atherosclerosis or myocardial  
 CC infarction), endocrine disorders (e.g. Addison's disease or  
 CC corticosteroid deficiency), reproductive system disorders (e.g.  
 CC testicular atrophy or dysmenorrhea), gastrointestinal disorders (e.g.  
 CC dysphagia or irritable bowel syndrome), infectious diseases, and/or  
 CC cancerous diseases. The polynucleotides can also be used to aid wound  
 CC healing and epithelial cell proliferation. The present sequence  
 CC represents the amino acid sequence of a human signal transduction pathway  
 CC component  
 XX  
 SQ Sequence 492 AA;

Query Match 100.0%; Score 2550; DB 6; Length 492;  
 Best Local Similarity 100.0%; Pred. No. 5.4e-235;  
 Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 MSDVAIVKEGWLHKGRIYKTRPRYFLKNDGTFIGYKRPQDVQREAPLNFSVAQC 60  
 Db 13 MSDVAIVKEGWLHKGRIYKTRPRYFLKNDGTFIGYKRPQDVQREAPLNFSVAQC 72  
 Qy 61 QLMKTERPRNTFIIRCLQWTTVIERTFHVETPEERBEWTTAQTVDGLKQEEEMDF 120  
 Db 73 QLMKTERPRNTFIIRCLQWTTVIERTFHVETPEERBEWTTAQTVDGLKQEEEMDF 132  
 Qy 121 RSGSPSDNSGAEMEVSIAKPKHRVTWNEPEYLLKLGKTFGKVLVKEKATGRYAMKI 180  
 Db 133 RSGSPSDNSGAEMEVSIAKPKHRVTWNEPEYLLKLGKTFGKVLVKEKATGRYAMKI 192  
 Qy 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFTQTHDRLCFVMEYANGGELPFHLS 240  
 Db 193 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFTQTHDRLCFVMEYANGGELPFHLS 252  
 Qy 241 RERVESDRARFYGAIEVSALDYLHSEKNVYVYRDILKLENMLDKDGHIKITDFGLCKEGI 300  
 Db 253 RERVESDRARFYGAIEVSALDYLHSEKNVYVYRDILKLENMLDKDGHIKITDFGLCKEGI 312  
 Qy 301 KDGATMTKTCGTPYLAPEVLENDYGRAVDWGLGVVYEMMCGRLPFYVQDHEKLFEL 360  
 Db 313 KDGATMTKTCGTPYLAPEVLENDYGRAVDWGLGVVYEMMCGRLPFYVQDHEKLFEL 372  
 Qy 361 ILMEERFPRTLGPPEAKSLLSGLLKQPKQRLGGGSEDAKEIMQHRFFAGIVQHVYEEK 420  
 Db 373 ILMEERFPRTLGPPEAKSLLSGLLKQPKQRLGGGSEDAKEIMQHRFFAGIVQHVYEEK 432  
 Qy 421 LSPFPKQVTSSETTRVDEEFTAQMITITPPDQDSDMECVDSRRRPHFPQFSYASGTA 480  
 Db 433 LSPFPKQVTSSETTRVDEEFTAQMITITPPDQDSDMECVDSRRRPHFPQFSYASGTA 492

RESULT 2  
 AA17972  
 ID AA17972 standard; protein; 480 AA.

XX  
 AC AA17972;  
 XX  
 DT 12-DEC-1997 (first entry)  
 XX  
 DE Human RAC protein kinase alpha.  
 XX  
 KW RAC protein kinase C-terminal binding protein; CTBP; modulator;

KW signal transduction; insulin; diabetes; cell proliferation; glycogen;  
 KW therapy; diagnosis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9718303-A1.  
 XX  
 PD 22-MAY-1997.  
 XX  
 PP 05-NOV-1996; 96WO-EP004810.  
 XX  
 PR 16-NOV-1995; 95GB-00023379.  
 PR 15-DEC-1995; 95GB-00025704.  
 XX  
 PA (NOVS ) NOVARTIS AG.  
 XX  
 PI Hemmings BA;  
 XX  
 DR WPI; 1997-289279/26.  
 DR N-PSDB; AAT67135.  
 XX  
 PT RAC protein kinase, or modulator excluding wortmannin and vanadate, for  
 PT use as medicament - and screening potential modulators of insulin  
 PT mediated intracellular signalling using RAC-PK, or fragment.  
 XX  
 PS Claim 1; Page 30-32; 38pp; English.  
 XX  
 CC This polypeptide sequence comprises human RAC protein kinase alpha (RAC-  
 CC PK), a protein directly involved in the inactivation of glycogen  
 CC synthetase kinase-3 and the activation of IMP dehydrogenase and in the  
 CC regulation of insulin-dependent signalling pathways, which control  
 CC cellular proliferation. RAC-PK and its fragments and modulators are  
 CC claimed for use as medicaments for the treatment of diseases involving  
 CC abnormalities in processes modulated by insulin, such as cellular  
 CC proliferation, insulin deficiency and/or excess blood sugar levels. RAC-  
 CC PK can also be used in a claimed method for screening potential  
 CC modulators of insulin-mediated intracellular signalling. Activated mutant  
 CC RAC-PKs (see AAW17983-85) may also be used in such screenings  
 XX  
 SQ Sequence 480 AA;

Query Match 99.8%; Score 2544; DB 2; Length 480;  
 Best Local Similarity 99.8%; Pred. No. 1.9e-234;  
 Matches 479; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSDVAIVKEGWLHKGRIYKTRPRYFLKNDGTFIGYKRPQDVQREAPLNFSVAQC 60  
 Db 1 MSDVAIVKEGWLHKGRIYKTRPRYFLKNDGTFIGYKRPQDVQREAPLNFSVAQC 60  
 Qy 61 QLMKTERPRNTFIIRCLQWTTVIERTFHVETPEERBEWTTAQTVDGLKQEEEMDF 120  
 Db 61 QLMKTERPRNTFIIRCLQWTTVIERTFHVETPEERBEWTTAQTVDGLKQEEEMDF 120  
 Qy 121 RSGSPSDNSGAEMEVSIAKPKHRVTWNEPEYLLKLGKTFGKVLVKEKATGRYAMKI 180  
 Db 121 RSGSPSDNSGAEMEVSIAKPKHRVTWNEPEYLLKLGKTFGKVLVKEKATGRYAMKI 180  
 Qy 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFTQTHDRLCFVMEYANGGELPFHLS 240  
 Db 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFTQTHDRLCFVMEYANGGELPFHLS 240  
 Qy 241 RERVESDRARFYGAIEVSALDYLHSEKNVYVYRDILKLENMLDKDGHIKITDFGLCKEGI 300  
 Db 241 RERVESDRARFYGAIEVSALDYLHSEKNVYVYRDILKLENMLDKDGHIKITDFGLCKEGI 300  
 Qy 301 KDGATMTKTCGTPYLAPEVLENDYGRAVDWGLGVVYEMMCGRLPFYVQDHEKLFEL 360  
 Db 301 KDGATMTKTCGTPYLAPEVLENDYGRAVDWGLGVVYEMMCGRLPFYVQDHEKLFEL 360  
 Qy 361 ILMEERFPRTLGPPEAKSLLSGLLKQPKQRLGGGSEDAKEIMQHRFFAGIVQHVYEEK 420  
 Db 361 ILMEERFPRTLGPPEAKSLLSGLLKQPKQRLGGGSEDAKEIMQHRFFAGIVQHVYEEK 420

This protein comprises human RAC protein kinase. The N-terminal pleckstrin homology (PH) domain of RAC protein kinase can be used in a claimed method for screening for modulators of signal pathways. This involves: (a) incubating the test compound with the PH domain of a signalling molecule which is capable of fluorescing; and (b) determining phospholipid-induced changes in fluorescence, indicating a functional interaction between the compound and the PH domain. Fluorescence is preferably associated with the Trp-223 of RAC protein kinase PH domain. The method allows screening for compounds which modulate signal pathways involving the serine/threonine kinase RAC and can especially be applied to protein kinases and their substrates, which are implicated in intracellular signalling and growth control. The high affinity binding of phospholipid to the PH domain of signalling molecules suggests that this domain is a membrane anchor for the molecules: molecule interactions with the cell membrane are important for their stable interaction with membrane-bound partners in signalling pathways, so that disruption of the interaction modulates the signalling effect. By measuring this modulation (which may be down-regulation for stimulatory interactions or upregulation for inhibitory interactions) compounds which can have an effect can be identified e.g. agents which cause conformational changes in the PH domains or which compete directly for binding of the PH domain to the cell membrane. A claimed method for production of the RAC protein kinase PH domain in a bacterial cell comprises expressing a nucleic acid sequence encoding the PH domain having at least 3 hydrophilic amino acids (preferably Lys) residues joined directly at its C-terminus (see AA0118519).

PT Identifying compounds which modulate expression of nucleic acids, used to  
 PT provide compounds having defined physical, chemical or bioactive  
 PT properties, e.g. antisense activity.

PS Example 29; Page 248-251; 264pp; English.

XX A method has been developed of defining a set of compounds that modulate  
 CC the expression of a target nucleic acid (tNA) sequence via binding of the  
 CC compounds with the tNA sequence. The method comprises generating a  
 CC library of virtual compounds in silico according to defined criteria, and  
 CC evaluating in silico the binding of the virtual compounds with the tNA  
 CC according to defined criteria. Also described are: (1) a method of  
 CC defining a set of oligonucleotides (ONs) that modulate the expression of  
 CC a tNA sequence via binding of the ONs with the tNA sequence comprising  
 CC generating a library of virtual compounds in silico according to defined  
 CC criteria, and evaluating in silico the binding of the virtual ONs with  
 CC the tNA according to defined criteria; and (2) a method of defining a set  
 CC of compounds that modulate the expression of a tNA sequence via binding  
 CC of the compounds with the tNA. The methods can be used for the generation  
 CC and identification of synthetic compounds having defined physical,  
 CC chemical or bioactive properties. Information gathered from assays of  
 CC such compounds is used to identify nucleic acid sequences that are  
 CC tractable to a variety of nucleotide sequence-based technologies, e.g.  
 CC antisense drug discovery and target validation. AA240852 to AA241220, and  
 CC AAY52701 to AAY52706, represent sequences used in the exemplification of  
 CC the present invention

XX Sequence 480 AA;

Query Match 99.8%; Score 2544; DB 2; Length 480;

Best Local Similarity 99.8%; Pred. No. 1.9e-234;

Matches 479; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	MSDVAIVKEGWLHKGGEYIKTWPRYFLKNDGTFIGYKERPDVDQREAPLNFSVAQC	60
Db	1	MSDVAIVKEGWLHKGGEYIKTWPRYFLKNDGTFIGYKERPDVDQREAPLNFSVAQC	60
Qy	61	QLMKTERPRNTFIIRCLQWTTVIERTFHVETPEEREETTAIQTVDGLKKQEEBEMDF	120
Db	61	QLMKTERPRNTFIIRCLQWTTVIERTFHVETPEEREETTAIQTVDGLKKQEEBEMDF	120
Qy	121	RSGSPSDNSGAEEMVSLAKPKHRTVMNEPEYLLKLGKTFGKVLVKEKATGRYYAMKI	180
Db	121	RSGSPSDNSGAEEMVSLAKPKHRTVMNEPEYLLKLGKTFGKVLVKEKATGRYYAMKI	180
Qy	181	LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLS	240
Db	181	LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLS	240
Qy	241	RERVSEDRARFYGAIEVSALDYHSEKNVYVRDLKLENMLDKDGHKIKITDFGLCKEGI	300
Db	241	RERVSEDRARFYGAIEVSALDYHSEKNVYVRDLKLENMLDKDGHKIKITDFGLCKEGI	300
Qy	301	KDGMATKTFCGTPEYLAPEVLENDYGRAVDWGLGVVMYEMMCGRLPFFYNQDHEKLFEL	360
Db	301	KDGMATKTFCGTPEYLAPEVLENDYGRAVDWGLGVVMYEMMCGRLPFFYNQDHEKLFEL	360
Qy	361	ILMEEIRFPRTLGPPEAKSLLSGLLKDPKQRLGGSGSDAKEIMQHRFFAGIVMWHVYEKK	420
Db	361	ILMEEIRFPRTLGPPEAKSLLSGLLKDPKQRLGGSGSDAKEIMQHRFFAGIVMWHVYEKK	420
Qy	421	LSPPFPKQVTSSETDTRYFDEEFTAQMITITPPDQDDSMCEVDSERRRPHFPQFSYASGTA	480
Db	421	LSPPFPKQVTSSETDTRYFDEEFTAQMITITPPDQDDSMCEVDSERRRPHFPQFSYASGTA	480

RESULT 5

AA33999

ID AA33999 standard; protein; 480 AA.

XX AA33999;

AC AA33999;

XX 26-NOV-1999 (first entry)

XX Human Akt-1 protein sequence.

XX DB

KW Human; Akt-1; antisense; diagnostic; therapeutic; prophylaxis; infection;  
 inflammation; tumor formation.

XX Homo sapiens.

XX US5958773-A.

XX 28-SEP-1999.

XX 17-DEC-1998; 98US-00212771.

XX 17-DEC-1998; 98US-00212771.

XX (ISIS-) ISIS PHARM INC.

XX Monia BP, Cowseert LM;

XX WPI; 1999-561048/47.

XX N-PSDB; AA222190.

XX Antisense compounds complementary to Akt-1 useful for, e.g. diagnostics,  
 PT therapeutics and as research reagents.

XX Example 13; Col 43-46; 32pp; English.

XX The invention provides antisense compounds of 8-30 nucleotides that  
 CC inhibit the expression of human Akt-1. The antisense compounds may be  
 CC used for diagnostics, therapeutics (for modulating the expression of Akt-  
 CC 1), prophylaxis (e.g. to prevent or delay infection, inflammation, or  
 CC tumor formation), as research reagents (e.g. to distinguish between  
 CC members of a biological pathway) and in kits. The present sequence  
 CC represents the human Akt-1 protein sequence

XX Sequence 480 AA;

Query Match 99.8%; Score 2544; DB 2; Length 480;

Best Local Similarity 99.8%; Pred. No. 1.9e-234;

Matches 479; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	MSDVAIVKEGWLHKGGEYIKTWPRYFLKNDGTFIGYKERPDVDQREAPLNFSVAQC	60
Db	1	MSDVAIVKEGWLHKGGEYIKTWPRYFLKNDGTFIGYKERPDVDQREAPLNFSVAQC	60
Qy	61	QLMKTERPRNTFIIRCLQWTTVIERTFHVETPEEREETTAIQTVDGLKKQEEBEMDF	120
Db	61	QLMKTERPRNTFIIRCLQWTTVIERTFHVETPEEREETTAIQTVDGLKKQEEBEMDF	120
Qy	121	RSGSPSDNSGAEEMVSLAKPKHRTVMNEPEYLLKLGKTFGKVLVKEKATGRYYAMKI	180
Db	121	RSGSPSDNSGAEEMVSLAKPKHRTVMNEPEYLLKLGKTFGKVLVKEKATGRYYAMKI	180
Qy	181	LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLS	240
Db	181	LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLS	240
Qy	241	RERVSEDRARFYGAIEVSALDYHSEKNVYVRDLKLENMLDKDGHKIKITDFGLCKEGI	300
Db	241	RERVSEDRARFYGAIEVSALDYHSEKNVYVRDLKLENMLDKDGHKIKITDFGLCKEGI	300
Qy	301	KDGMATKTFCGTPEYLAPEVLENDYGRAVDWGLGVVMYEMMCGRLPFFYNQDHEKLFEL	360
Db	301	KDGMATKTFCGTPEYLAPEVLENDYGRAVDWGLGVVMYEMMCGRLPFFYNQDHEKLFEL	360
Qy	361	ILMEEIRFPRTLGPPEAKSLLSGLLKDPKQRLGGSGSDAKEIMQHRFFAGIVMWHVYEKK	420
Db	361	ILMEEIRFPRTLGPPEAKSLLSGLLKDPKQRLGGSGSDAKEIMQHRFFAGIVMWHVYEKK	420
Qy	421	LSPPFPKQVTSSETDTRYFDEEFTAQMITITPPDQDDSMCEVDSERRRPHFPQFSYASGTA	480
Db	421	LSPPFPKQVTSSETDTRYFDEEFTAQMITITPPDQDDSMCEVDSERRRPHFPQFSYASGTA	480





CC It is therefore also useful for treating muscular dystrophy, spinal  
 CC muscular atrophy, anabolic steroid-induced muscle injury, skeletal  
 CC oxidative stress, physical exercise and unloading-induced skeletal muscle  
 CC atrophy. The Akt protein can also be used in screening for an inhibitory  
 CC agent that inhibits apoptotic cell-death of cells  
 XX  
 SQ Sequence 480 AA;

Query Match 99.8%; Score 2544; DB 3; Length 480;  
 Best Local Similarity 99.8%; Pred. No. 1.9e-234;  
 Matches 479; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSDVAIVKEGWLHKGRIYKTRPRYFLNKGDTFGYKRPQDVQREAPLNFSVAQC 60  
 Db 1 MSDVAIVKEGWLHKGRIYKTRPRYFLNKGDTFGYKRPQDVQREAPLNFSVAQC 60  
 Qy 61 QLMKTERPRNTFIIRCLQWTVIERTFHVETPEEREWTAIQTVDGLKQEEEMDF 120  
 Db 61 QLMKTERPRNTFIIRCLQWTVIERTFHVETPEEREWTAIQTVDGLKQEEEMDF 120  
 Qy 121 RSGSPDNGSAAEEMVSLAKPKHRVTWNEPEYLLKLGKTFGKVLVKEKATGRYYAMKI 180  
 Db 121 RSGSPDNGSAAEEMVSLAKPKHRVTWNEPEYLLKLGKTFGKVLVKEKATGRYYAMKI 180  
 Qy 181 LKKEVIVAKDEVATHTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELPFHLS 240  
 Db 181 LKKEVIVAKDEVATHTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELPFHLS 240  
 Qy 241 RERVSEDRARFYGAIEVSALDYHSEKNVYRDLENLMDKDGHIKITDGLCKEGI 300  
 Db 241 RERVSEDRARFYGAIEVSALDYHSEKNVYRDLENLMDKDGHIKITDGLCKEGI 300  
 Qy 301 KDGATMTKTCGTPPEYLAPEVLENDYGRAVDWGLGVVYEMMCGRLPFYVQDHEKLFEL 360  
 Db 301 KDGATMTKTCGTPPEYLAPEVLENDYGRAVDWGLGVVYEMMCGRLPFYVQDHEKLFEL 360  
 Qy 361 ILMBEIRFPRTLGPPEAKSLLSGLLKQPKQRLGGGSDAKEIMQHRFFAGIVQHVEKK 420  
 Db 361 ILMBEIRFPRTLGPPEAKSLLSGLLKQPKQRLGGGSDAKEIMQHRFFAGIVQHVEKK 420  
 Qy 421 LSPFPKQVTSSETDTRYFDEEFTAQMITITPPQDDSMCECVDSERRPHFPQFSYASGTA 480  
 Db 421 LSPFPKQVTSSETDTRYFDEEFTAQMITITPPQDDSMCECVDSERRPHFPQFSYASGTA 480

RESULT 8  
 AAG78020  
 ID AAG78020 standard; protein; 480 AA.  
 XX AC AAG78020;  
 XX AC AAG78020;  
 DT 31-JAN-2002 (first entry)  
 XX DE Human Akt1.  
 XX DE Human Akt1.  
 KW Human; Akt3; AH/PH-domain containing serine/threonine kinase; Akt;  
 KW cerebroprotective; neurotropic; hepatotrophic; antiarthritic;  
 KW osteopathic; vasotrophic; hepatotrophic; inhibitor of apoptosis; ASK1;  
 KW apoptosis stimulating kinase 1; hypoxia; necrosis; myocardial infarction;  
 KW ischaemia reperfusion injury; stroke; organ transplantation;  
 KW coronary artery bypass; tumour cell survival; gene therapy;  
 KW Alzheimer's disease; osteoarthritis; Akt1.  
 XX OS Homo sapiens.  
 XX PN W0200168850-A2.  
 XX PD 20-SEP-2001.  
 XX PF 09-MAR-2001; 2001WO-US007663.  
 XX PR 14-MAR-2000; 2000US-00526043.

PA (AVET ) AVENTIS PHARM PROD INC.  
 XX Guo K, Pagnoni MF, Clark KL, Ivashchenko VD;  
 XX WPI; 2001-582452/65.  
 DR New nucleic acid encoding human Akt3 protein, useful for inhibiting cell  
 PT death and treating myocardial infarction, ischemia reperfusion injury  
 PT associated with stroke, liver damage and renal failure.  
 XX  
 PS Example 1; Fig 1; 73pp; English.

CC The invention relates to human Akt3 protein (AH/PH-domain containing  
 CC serine/threonine kinase, Akt) comprising a fully defined sequence  
 CC (AAG78018) of 465 amino acids, its splice variant or allelic variant,  
 CC where the encoding polynucleotide hybridizes under stringent conditions  
 CC with a nucleic acid containing a nucleotide sequence (AAH79025) of 1570  
 CC base pairs defined in the specification. Akt3 has cerebroprotective,  
 CC neurotropic, hepatotrophic, antiarthritic, osteopathic, vasotrophic and  
 CC hepatotrophic activity, as an inhibitor of apoptosis and/or apoptosis  
 CC stimulating kinase 1 (ASK1)-induced cell death. Akt3 operably linked to a  
 CC regulatory region is useful for inhibiting cell death in cardiac myocytes  
 CC resulting from hypoxia, apoptosis or necrosis and for treating myocardial  
 CC infarction or ischaemia reperfusion injury, particularly that associated  
 CC with stroke, liver damage, renal failure, organ transplantation or  
 CC coronary artery bypass grafting. Agonist of Akt3 are useful for improving  
 CC Akt3 activity during treatment of patients suffering from myocardial  
 CC infarction or ischaemia reperfusion injury and inhibitors of Akt3  
 CC activity decrease tumour cell survival and result in tumour regression.  
 CC Akt3 protects cells from apoptosis. Gene therapy using Akt3 reduces the  
 CC quantity of cell death and final infarct size, resulting in improved post  
 CC -infarction function, improved quality of life and reduced mortality. In  
 CC patients with existing heart failure, gene therapy with Akt3 retards the  
 CC process of ventricular dilation and slows down disease progression. Akt3  
 CC gene therapy is useful for treating other disease states, involving cell  
 CC death by apoptosis, including Alzheimer's disease, liver degeneration or  
 CC osteoarthritis. The present sequence is that of the human Akt1 protein

SQ Sequence 480 AA;

Query Match 99.8%; Score 2544; DB 4; Length 480;  
 Best Local Similarity 99.8%; Pred. No. 1.9e-234;  
 Matches 479; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSDVAIVKEGWLHKGRIYKTRPRYFLNKGDTFGYKRPQDVQREAPLNFSVAQC 60  
 Db 1 MSDVAIVKEGWLHKGRIYKTRPRYFLNKGDTFGYKRPQDVQREAPLNFSVAQC 60  
 Qy 61 QLMKTERPRNTFIIRCLQWTVIERTFHVETPEEREWTAIQTVDGLKQEEEMDF 120  
 Db 61 QLMKTERPRNTFIIRCLQWTVIERTFHVETPEEREWTAIQTVDGLKQEEEMDF 120  
 Qy 121 RSGSPDNGSAAEEMVSLAKPKHRVTWNEPEYLLKLGKTFGKVLVKEKATGRYYAMKI 180  
 Db 121 RSGSPDNGSAAEEMVSLAKPKHRVTWNEPEYLLKLGKTFGKVLVKEKATGRYYAMKI 180  
 Qy 181 LKKEVIVAKDEVATHTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELPFHLS 240  
 Db 181 LKKEVIVAKDEVATHTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELPFHLS 240  
 Qy 241 RERVSEDRARFYGAIEVSALDYHSEKNVYRDLENLMDKDGHIKITDGLCKEGI 300  
 Db 241 RERVSEDRARFYGAIEVSALDYHSEKNVYRDLENLMDKDGHIKITDGLCKEGI 300  
 Qy 301 KDGATMTKTCGTPPEYLAPEVLENDYGRAVDWGLGVVYEMMCGRLPFYVQDHEKLFEL 360  
 Db 301 KDGATMTKTCGTPPEYLAPEVLENDYGRAVDWGLGVVYEMMCGRLPFYVQDHEKLFEL 360  
 Qy 361 ILMBEIRFPRTLGPPEAKSLLSGLLKQPKQRLGGGSDAKEIMQHRFFAGIVQHVEKK 420  
 Db 361 ILMBEIRFPRTLGPPEAKSLLSGLLKQPKQRLGGGSDAKEIMQHRFFAGIVQHVEKK 420  
 Qy 421 LSPFPKQVTSSETDTRYFDEEFTAQMITITPPQDDSMCECVDSERRPHFPQFSYASGTA 480

3

Query Match	99.8%; Score 2544; DB 4; Length 480;	PS	Disclosure; Page 47-48; 53pp; English.
Best Local Similarity	99.8%; Pred. No. 1.9e-234;	XX	The invention relates to identifying an agent modulating interaction
Matches 479; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		CC	between integrin-linked kinase (ILK) and presenilin-1 (PS1) comprising
		CC	providing ILK, PS1 or their functional variants, as first and second
		CC	components respectively, contacting the components in the presence of a
		CC	test agent under conditions that in absence of the agent, would permit
		CC	the components to interact and determining whether the agent is capable
		CC	of modulating the interaction between the components. Also included are
		CC	the method above where the components are protein kinase beta (PKB),
		CC	gamma secretase or their functional variants, test kits for carrying out
		CC	the methods and an agent identified by the methods. The methods are used
		CC	for identifying an agent that modulates interaction between ILK and PS1.
		CC	or PKB or gamma-secretase. The agent has therapeutic applications in
		CC	treating humans or animals, for treating a host suffering from a
		CC	condition associated with an interaction between ILK and PS1, activity of
		CC	PKB, activity of gamma-secretase, apoptosis, cancer and Alzheimer's
		CC	disease. The agent is also useful for manufacturing a medicament for use
		CC	in treatment of the above mentioned conditions. The present sequence
		CC	represents human protein kinase B alpha
		XX	
SQ	Sequence 480 AA;		
Query Match	99.8%; Score 2544; DB 5; Length 480;		
Best Local Similarity	99.8%; Pred. No. 1.9e-234;		
Matches 479; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			
Qy	1 MSDVAIVKEGWLKRGGEYIKTWPRYFLLKNDGTFIGYKERPDVDQREAPLNFSVAQC 60		
Db	1 MSDVAIVKEGWLKRGGEYIKTWPRYFLLKNDGTFIGYKERPDVDQREAPLNFSVAQC 60		
Qy	61 QLMKTERPRNTFIIRCLQWTTVIERTFHVETPEEREETTAQTVDGLKKQEEEMDF 120		
Db	61 QLMKTERPRNTFIIRCLQWTTVIERTFHVETPEEREETTAQTVDGLKKQEEEMDF 120		
Qy	121 RSGSPDNGSGAEEMVSLAKPKHRVTWNEPEYLLKLGKGTGKVLVKEKATGRYYAMKI 180		
Db	121 RSGSPDNGSGAEEMVSLAKPKHRVTWNEPEYLLKLGKGTGKVLVKEKATGRYYAMKI 180		
Qy	181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLS 240		
Db	181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLS 240		
Qy	241 RERVSEDRARFYGAIEVSALDYLHSEKNVYVYRDLEMLDKDGHIKITDFGLCKEGI 300		
Db	241 RERVSEDRARFYGAIEVSALDYLHSEKNVYVYRDLEMLDKDGHIKITDFGLCKEGI 300		
Qy	301 KDGATMKTFCGTPPYLAPEVLENDYGRAVDWGLGVVYVYEMMCGRLPFYVNDHEKLFEL 360		
Db	301 KDGATMKTFCGTPPYLAPEVLENDYGRAVDWGLGVVYVYEMMCGRLPFYVNDHEKLFEL 360		
Qy	361 ILMEEIRFPRTLGPPEAKSLLSGLLKDPKQRLGGSGSDAKEIMQHRFFAGIVMHOVVEKK 420		
Db	361 ILMEEIRFPRTLGPPEAKSLLSGLLKDPKQRLGGSGSDAKEIMQHRFFAGIVMHOVVEKK 420		
Qy	421 LSPFPKQVTSSETDTRYFDEEFTAQMTITPPDQDDSMCEVDSERRPFPQFSYSASSTA 480		
Db	421 LSPFPKQVTSSETDTRYFDEEFTAQMTITPPDQDDSMCEVDSERRPFPQFSYSASSTA 480		
RESULT 11			
AAU79418			
ID	AAU79418 standard; protein; 480 AA.		
XX			
AC	AAU79418;		
XX			
DT	02-JUL-2002 (first entry)		
XX			
DE	Human protein kinase B alpha.		
XX			
KW	Human; integrin-linked kinase; ILK; presenilin-1; protein kinase B; PKB;		
KW	gamma secretase; apoptosis; Alzheimer's disease; PS-1; neurotropic;		
KW	neuroprotective; cytostatic; cancer.		
XX			
OS	Homo sapiens.		
XX			
FN	WO200222862-A2.		
XX			
PD	21-MAR-2002.		
XX			
PF	12-SEP-2001; 2001WO-GB004094.		
XX			
PR	12-SEP-2000; 2000GB-00022333.		
XX			
PA	(GLAX ) GLAXO GROUP LTD.		
XX			
PI	Hiles ID, Ellis C;		
XX			
DR	WPT; 2002-351896/38.		
XX			
PT	Identifying agent that modulates interaction between integrin-linked		
PT	kinase and presenilin-1, useful for treating Alzheimer's disease, and		
PT	identifying agent that modulates protein kinase B or gamma secretase		
PT	activity.		
XX			

nonhyperlipidaemic; hypertension; vascular disease; gangrene; wound;  
 Buerger's syndrome; myocardial infarction; coronary artery disease;  
 ischaemia.

Homo sapiens.

Key Location/Qualifiers  
 Domain 5..108  
 /label= PH domain  
 /note= "Pleckstrin homology domain"  
 Domain 150..408  
 /note= "Kinase domain"  
 Modified-site 308  
 /note= "Phosphorylation site"  
 Modified-site 473  
 /note= "Phosphorylation site"

WO200193806-A2.  
 13-DEC-2001.  
 05-JUN-2001; 2001WO-US018175.  
 08-JUN-2000; 2000US-00590740.  
 (SELI-) ST ELIZABETH'S MEDICAL CENT BOSTON INC.  
 Walsh K;  
 WPI; 2002-164293/21.  
 N-PSDB; AAD28548.

Use of 3-hydroxy-3-methylglutaryl-coenzyme A reductase inhibitor in  
 promoting angiogenesis in a tissue of a subject to treat conditions e.g.  
 hypertension.

Disclosure; Page 66-67; 70pp; English.

The invention relates to 3-hydroxy-3-methylglutaryl-coenzyme A (HMG-CoA)  
 reductase inhibitors and their use in promoting angiogenesis and in  
 activating Akt polypeptides in vascular endothelial cells. Akt is a proto-  
 oncogene encoding a serine-threonine kinase (also known as protein  
 kinase B, PKB). The invention also relates to methods and compositions  
 for the treatment of conditions associated with vascular insufficiency.  
 HMG-CoA reductase inhibitors are used for treating nonhyperlipidaemic and  
 /or nonhypercholesterolaemic subjects who are in need of increased blood  
 flow to a tissue or promoting angiogenesis, to treat conditions such as  
 hypertension, diabetic peripheral vascular disease, gangrene, Buerger's  
 syndrome, wound (e.g. surgical wound), ischaemia of the muscle, brain,  
 kidney, lung, heart and limb, severe occlusive and/or obstructive  
 vascular disease, peripheral vascular disease, myocardial ischaemia,  
 myocardial infarction, coronary artery disease, cerebral vascular disease  
 and visceral vascular disease. The present sequence is human Akt protein

Sequence 480 AA;  
 Query Match 99.8%; Score 2544; DB 5; Length 480;  
 Best Local Similarity 99.8%; Pred. No. 1.9e-234;  
 Matches 479; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 MSDVAIVKEGWLHKRGEYIKTWPRYFLKNDGTFIGYKRPQDVDDQREAPLNFSVAQC 60  
 1 MSDVAIVKEGWLHKRGEYIKTWPRYFLKNDGTFIGYKRPQDVDDQREAPLNFSVAQC 60  
 61 QLMKTERPNTFIIRCLQWTVIERTFHVTPPEREWTTAIQTVADGLKKQEEEMDF 120  
 61 QLMKTERPNTFIIRCLQWTVIERTFHVTPPEREWTTAIQTVADGLKKQEEEMDF 120  
 121 RSGSPSDNSGAEEMVSLAKPKHRVTWMEFYLLKLGKGTGKVLVKEKATGRYAMKI 180  
 121 RSGSPSDNSGAEEMVSLAKPKHRVTWMEFYLLKLGKGTGKVLVKEKATGRYAMKI 180  
 181 LKKEVIVAKDEVVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLS 240

Db 181 LKKEVIVAKDEVVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLS 240  
 Qy 241 RERVFSSEDRARFYGAETVSALDYHLSEKNVYVYRDLEKLENMLDKDGHKIKITDFGLCKEGI 300  
 Db 241 RERVFSSEDRARFYGAETVSALDYHLSEKNVYVYRDLEKLENMLDKDGHKIKITDFGLCKEGI 300  
 Qy 301 KDGMTKTCGTPEYLAPEVLENDNDYGRVDWGLGVVYEMMCGRLPFFYNQDHEKLPFEL 360  
 Db 301 KDGMTKTCGTPEYLAPEVLENDNDYGRVDWGLGVVYEMMCGRLPFFYNQDHEKLPFEL 360  
 Qy 361 ILMEEIFRPTLGPPEAKSLLSGLLKDPKORLGGGSEDAKEIMQHRFFAGVWQHVYKK 420  
 Db 361 ILMEEIFRPTLGPPEAKSLLSGLLKDPKORLGGGSEDAKEIMQHRFFAGVWQHVYKK 420  
 Qy 421 LSPPFKQVTSSETTRYDFDEFTAQMITITPPDQDDSMCEVDSERRRHPFPQFSASGTA 480  
 Db 421 LSPPFKQVTSSETTRYDFDEFTAQMITITPPDQDDSMCEVDSERRRHPFPQFSASGTA 480

RESULT 13  
 ABB06996  
 ID ABB06996 standard; protein; 480 AA.  
 XX AC ABB06996;  
 XX DT 20-JUN-2002 (first entry)  
 XX DE Human Akt1 protein SEQ ID NO:5.  
 XX KW Human; Hsp90 beta; Hsp90 alpha; Akt1; Akt2; Akt3; apoptosis regulation;  
 KW apoptosis; serine/threonine kinase; heat shock protein; anticancer;  
 KW cytosolic; cardiac; vasotropic; hepatotropic; neuroprotective;  
 KW antidiabetic; neurotropic; cancer; diabetes; Alzheimer's disease;  
 KW cell death; radiation; brain ischaemia; cardiac ischaemia.  
 XX OS Homo sapiens.  
 XX PN WO200215925-A1.  
 XX PD 28-FEB-2002.  
 XX PF 22-AUG-2001; 2001WO-JP007179.  
 XX PR 22-AUG-2000; 2000JP-00251529.  
 XX PA (KYOW) KYOWA HAKKO KOGYO KK.  
 XX TSURUO T. TSURUO T.  
 XX PI Tsuruo T, Fujita N, Sato S;  
 XX WPI; 2002-292035/33.  
 XX DR N-PSDB; ABL50837.  
 XX PT Regulation of apoptosis by promoting or inhibiting the intracellular  
 binding of Akt with Hsp90, useful for prevention and treatment of  
 apoptosis-regulation associated diseases including cancer.  
 XX PS Claim 12; Page 76-78; 93pp; Japanese.  
 CC The present invention describes the regulation of apoptosis, in which the  
 intracellular binding of Akt (a serine/threonine kinase) with Hsp90 (a  
 heat-shock protein) is promoted or inhibited. The present invention also  
 describes: (1) isoforms of Akt and Hsp90, and their partial peptides  
 including the binding domain; (2) antibodies to Akt or Hsp90; (3) DNA  
 encoding Akt or Hsp90 or their partial peptides including the binding  
 domain; (4) expression vectors containing the DNA; (5) host cells  
 transformed by the vectors; (6) production of Akt or Hsp90 or their  
 partial peptides including the binding domain by culture of the  
 transformed cells; (7) screening compounds for their ability to modify  
 intracellular Akt activity by contact with cells expressing Akt or Hsp90;  
 and (8) drug compositions containing antibodies recognizing the binding  
 domain of Akt or Hsp90 and optionally also an anticancer agent. Akt and

CC Hsp90 have cytosolic, cardiac, vasotropic, hepatotropic, antidiabetic,  
CC neuroprotective and neurotropic activities. Blockade of the binding of  
CC Hsp90 with Akt increases the sensitivity of cells to apoptosis induction.  
CC Akt and Hsp90 can be used in the prevention and treatment of diseases  
CC with which apoptosis regulation is associated, including cancer (such as  
CC gastric cancer, ovarian cancer, breast cancer, pancreatic cancer and  
CC prostate cancer), diabetes, Alzheimer's disease, cell death caused by  
CC radiation or anticancer agents, brain ischaemia or cardiac ischaemia. The  
CC present sequence represents human Akt1 which is used in the  
CC exemplification of the present invention

XX  
SQ Sequence 480 AA;  
Query Match 99.8%; Score 2544; DB 5; Length 480;  
Best Local Similarity 99.8%; Pred. No. 1.9e-234;  
Matches 479; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSDVAIVKGEWHLKRGYIKTWPRYFLKNDGTFIGYKRPQDVQREAPLNFSVAQC 60  
Db 1 MSDVAIVKGEWHLKRGYIKTWPRYFLKNDGTFIGYKRPQDVQREAPLNFSVAQC 60  
Qy 61 QLMKTERPRNTFIIRCLQWTVIERTFHVETPEEREETTAQTQVADGLKKQEEEMDF 120  
Db 61 QLMKTERPRNTFIIRCLQWTVIERTFHVETPEEREETTAQTQVADGLKKQEEEMDF 120  
Qy 121 RSGSPSDNSGAEEMVSLAKPKHRTWNEPEYLLKLGKTFGKVLVKEKATGRYYAMKI 180  
Db 121 RSGSPSDNSGAEEMVSLAKPKHRTWNEPEYLLKLGKTFGKVLVKEKATGRYYAMKI 180  
Qy 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLS 240  
Db 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLS 240  
Qy 241 RERVSEDRARFYGAIEVSALDYHSEKNVYVRDLKLENMLDKDGHKIKITDGLCKEGI 300  
Db 241 RERVSEDRARFYGAIEVSALDYHSEKNVYVRDLKLENMLDKDGHKIKITDGLCKEGI 300  
Qy 301 KDGATMKTFCGTPPEYLAPEVLEDNDYGRAVDWGLGVVYEMMCGRLPFYNQDHEKLFEL 360  
Db 301 KDGATMKTFCGTPPEYLAPEVLEDNDYGRAVDWGLGVVYEMMCGRLPFYNQDHEKLFEL 360  
Qy 361 ILMEERFPRTLGLPEAKSLLSGLLKQPKQKRLGGSEDAKEIMQHRFFAGIVQHVYVEKK 420  
Db 361 ILMEERFPRTLGLPEAKSLLSGLLKQPKQKRLGGSEDAKEIMQHRFFAGIVQHVYVEKK 420  
Qy 421 LSPFPKQVTSSETDTRYFDEEFTAQMITITPPDQDSDMECVDSRRRPHFPQFSYASGTA 480  
Db 421 LSPFPKQVTSSETDTRYFDEEFTAQMITITPPDQDSDMECVDSRRRPHFPQFSYASGTA 480

RESULT 14  
ABR57472  
ID ABR57472 standard; protein; 480 AA.  
XX  
AC ABR57472;  
XX  
DT 15-SEP-2003 (first entry)  
XX  
DE Human PKB-alpha amino acid sequence.

XX Protein kinase B; PKB/Akt; enzyme; crystal structure; drug discovery;  
KW protein co-ordinate data; cytosolic; antidiabetic; vasotropic; PKB;  
KW neurotropic; neuroprotective; gene therapy; protein kinase B beta; PKBbeta;  
KW structural analysis; cancer; diabetes; diabetes; erectile dysfunction; human;  
KW neurodegeneration.  
XX  
OS Homo sapiens.  
XX  
XX WO2003016516-A2.  
XX  
XX  
PD 27-FEB-2003.  
XX  
XX 14-AUG-2002; 2002WO-GB003735.

XX  
PR 14-AUG-2001; 2001GB-00019860.  
PR 01-MAY-2002; 2002GB-00009985.  
XX  
XX (NOVS ) NOVARTIS FORSCHUNGSSTIFTUNG ZWEIGNIEDERL.  
PA (CANC-) CANCER RES INST.  
XX  
PI Barford D, Yang J, Hemmings BA, Cron PD;  
XX  
XX WPI; 2003-268328/26.  
XX  
XX New crystal of protein kinase B beta, useful for activating protein  
PT kinases, e.g. AGC kinases, comprises three-dimensional atomic coordinates  
PT or a tetragonal space group.  
XX  
PS Disclosure; Fig 7; 284pp; English.

XX The present invention describes a crystal of protein kinase B beta  
CC (PKBbeta) comprising (i), where (i) comprises: (a) a tetragonal space  
CC group P4-1-2-1-2 and unit cell dimensions of: a = 149.33 plus or minus  
CC 0.5 Angstrom, b = 149.33 plus or minus 0.5 Angstrom, c = 39.77 plus or  
CC minus 0.5 Angstrom; a = 148.40 plus or minus 0.5 Angstrom, b = 148.40  
CC plus or minus 0.5 Angstrom, c = 38.55 plus or minus 0.5 Angstrom; a =  
CC 149.70 plus or minus 0.5 Angstrom, b = 149.70 plus or minus 0.5 Angstrom,  
CC c = 39.19 plus or minus 0.5 Angstrom; or a = 149.52 plus or minus 0.5  
CC Angstrom, b = 149.52 plus or minus 0.5 Angstrom, c = 39.06 plus or minus  
CC 0.5 Angstrom; or (b) the three-dimensional atomic coordinates listed in  
CC the specification. (i) has cytostatic, antidiabetic, vasotropic,  
CC neurotropic and neuroprotective activities, and can be used in gene  
CC therapy. The crystal of PKBbeta, and methods from the present invention,  
CC are useful in activating protein kinases, particularly AGC kinases, for  
CC identifying modulators of protein kinase activity, and for structural  
CC analysis of other protein kinases. The crystal may also be used in  
CC manufacturing a medicament for treating cancers, diabetes, erectile  
CC dysfunction or neurodegeneration. The present sequence represents the  
CC human PKB-alpha amino acid sequence, which is given in the  
CC exemplification of the present invention

XX Sequence 480 AA;  
SQ  
Query Match 99.8%; Score 2544; DB 6; Length 480;  
Best Local Similarity 99.8%; Pred. No. 1.9e-234;  
Matches 479; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSDVAIVKGEWHLKRGYIKTWPRYFLKNDGTFIGYKRPQDVQREAPLNFSVAQC 60  
Db 1 MSDVAIVKGEWHLKRGYIKTWPRYFLKNDGTFIGYKRPQDVQREAPLNFSVAQC 60  
Qy 61 QLMKTERPRNTFIIRCLQWTVIERTFHVETPEEREETTAQTQVADGLKKQEEEMDF 120  
Db 61 QLMKTERPRNTFIIRCLQWTVIERTFHVETPEEREETTAQTQVADGLKKQEEEMDF 120  
Qy 121 RSGSPSDNSGAEEMVSLAKPKHRTWNEPEYLLKLGKTFGKVLVKEKATGRYYAMKI 180  
Db 121 RSGSPSDNSGAEEMVSLAKPKHRTWNEPEYLLKLGKTFGKVLVKEKATGRYYAMKI 180  
Qy 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLS 240  
Db 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLS 240  
Qy 241 RERVSEDRARFYGAIEVSALDYHSEKNVYVRDLKLENMLDKDGHKIKITDGLCKEGI 300  
Db 241 RERVSEDRARFYGAIEVSALDYHSEKNVYVRDLKLENMLDKDGHKIKITDGLCKEGI 300  
Qy 301 KDGATMKTFCGTPPEYLAPEVLEDNDYGRAVDWGLGVVYEMMCGRLPFYNQDHEKLFEL 360  
Db 301 KDGATMKTFCGTPPEYLAPEVLEDNDYGRAVDWGLGVVYEMMCGRLPFYNQDHEKLFEL 360  
Qy 361 ILMEERFPRTLGLPEAKSLLSGLLKQPKQKRLGGSEDAKEIMQHRFFAGIVQHVYVEKK 420  
Db 361 ILMEERFPRTLGLPEAKSLLSGLLKQPKQKRLGGSEDAKEIMQHRFFAGIVQHVYVEKK 420  
Qy 421 LSPFPKQVTSSETDTRYFDEEFTAQMITITPPDQDSDMECVDSRRRPHFPQFSYASGTA 480

Db 421 LSPFPKQVTSSTDTTRYFDEEFTAQMITITPPDQDDSMCEVDSRRPHFPQFSASSTA 480

RESULT 15  
ADFI18630  
ID ADFI18630 standard; protein; 480 AA.  
XX ADFI18630;  
AC ADFI18630;  
XX 12-FEB-2004 (first entry)  
DT Human Akt kinase.  
XX Human; Akt; oncoprotein E7; cytostatic; gene therapy; kinase; enzyme.  
KW Homo sapiens.  
XX WO2003089922-A2.  
XX 30-OCT-2003.  
XX 21-APR-2003; 2003WO-US012667.  
XX 19-APR-2002; 2002US-0374245P.  
PR (UTRP ) UNIV ROCHESTER.  
PA Mccance D, Westbrook TF;  
XX WPI; 2003-845498/78.  
DR N-PSDB; ADFI18631.  
XX

Identifying a compound that inhibits E7 cellular proliferation activity by administering a compound to a system, where the system maintains Akt activity and selecting a compound that decreases the amount of Akt activity.  
PS Disclosure; SEQ ID NO 6; 119pp; English.

The present sequence is the protein sequence of human Akt. This is a kinase that phosphorylates p21Cip1 in the nuclear localisation signal of p21Cip1. Upon phosphorylation, nuclear transport does not occur and p21Cip1 is ubiquitinated and subsequently degraded. Human papillomavirus oncoprotein E7 abrogates Raf-associated arrest and prevents inhibition of cyclin E-CDK2 activity without disrupting Raf induction of p21Cip1. E7 neither interacts with p21Cip1 nor derepresses p21Cip1-associated CDK2 activity, but instead reduces the association between p21Cip1 and cyclin E-CDK2 complexes. Raf down-regulates steady-state levels of Akt, a regulator of p21Cip1 localisation, leading to loss of p21Cip1 phosphorylation and accumulation of p21Cip1. E7 disrupts the effects of Raf on Akt activity and prevents p21Cip1 nuclear accumulation. Maintenance of Akt activity is necessary and sufficient to bypass Raf arrest. The invention provides methods for identifying and using inhibitors of E7 cell proliferation activity, and for identifying and using compounds capable of promoting the nuclear localization of p21Cip1. The methods can be used to inhibit aberrant cellular proliferation for treatment of cancer.

Sequence 480 AA;  
Query Match 99.8%; Score 2544; DB 7; Length 480;  
Best Local Similarity 99.8%; Pred. No. 1.9e-234;  
Matches 479; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MSDVAIVKEGWLHKEGYIKTWPRYELLKNDGTFYGVKRPQDVDDQREAPLNFSVAQC 60  
DB 1 MSDVAIVKEGWLHKEGYIKTWPRYELLKNDGTFYGVKRPQDVDDQREAPLNFSVAQC 60  
QY 61 QLMKTERPRPNTFIIRCLQWTVIERTFHVETPEEREETWTAIQVADGLKKQEEEMDF 120  
DB 61 QLMKTERPRPNTFIIRCLQWTVIERTFHVETPEEREETWTAIQVADGLKKQEEEMDF 120

QY 121 RSGSPSDNSGAEEMEVSILAKPKHRVTWNEPEYLLGKGTGKVLVKEKATGRYYANKI 180  
DB 121 RSGSPSDNSGAEEMEVSILAKPKHRVTWNEPEYLLGKGTGKVLVKEKATGRYYANKI 180  
QY 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLS 240  
DB 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLS 240  
QY 241 RERVSEDRAFPYGAIEIVSALDYLHSEKNVYVYRDLKLENMLDKDGHIKITDFGLCKEGI 300  
DB 241 RERVSEDRAFPYGAIEIVSALDYLHSEKNVYVYRDLKLENMLDKDGHIKITDFGLCKEGI 300  
QY 301 KDGMTKTFCTGTPYLAPEVLENDYGRAVDWGLGVVYEMWCGRLPFYVQDHEKLFEL 360  
DB 301 KDGMTKTFCTGTPYLAPEVLENDYGRAVDWGLGVVYEMWCGRLPFYVQDHEKLFEL 360  
QY 361 ILMEIIRFPRTLGPPEAKSLLSGLLKOPKQRLGGSGSEDAKEIMQHRFPFAGIVMQHYEKK 420  
DB 361 ILMEIIRFPRTLGPPEAKSLLSGLLKOPKQRLGGSGSEDAKEIMQHRFPFAGIVMQHYEKK 420  
QY 421 LSPFPKQVTSSTDTTRYFDEEFTAQMITITPPDQDDSMCEVDSRRPHFPQFSASSTA 480  
DB 421 LSPFPKQVTSSTDTTRYFDEEFTAQMITITPPDQDDSMCEVDSRRPHFPQFSASSTA 480

Search completed: February 23, 2005, 20:45:26  
Job time : 168 secs



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